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L5: Entry 9 of 14

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Oct 3, 2002

DOCUMENT-IDENTIFIER: US 20020143159 A1

TITLE: BONE MORPHOGENETIC PROTEIN (BMP)-17 AND BMP-18 COMPOSITIONS

Summary of Invention Paragraph:

[0003] Human BMP-17 and BMP-18 appear to be human homologs of a murine protein called Lefty. The nucleotide and amino acid sequences of murine Lefty are described in Zhou et al., Nature, 361:543-547 (1993). The murine Lefty gene has been described as being expressed in the mouse node during gastrulation. A related human protein, designated endometrial bleeding associated factor [EBAF] was published in Kothapelli et al., J. Clin. Invest., 99:2342-2350 (1997).

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# O00292

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#### Entry information

Entry name **TGF4\_HUMAN**  
 Primary accession number **O00292**  
 Secondary accession numbers **O75611 Q8NBQ9**  
 Entered in Swiss-Prot in Release 35, November 1997  
 Sequence was last modified in Release 40, October 2001  
 Annotations were last modified in Release 44, July 2004

#### Name and origin of the protein

Protein name **Transforming growth factor beta 4 [Precursor]**  
 Synonyms **TGF-beta 4**, **Endometrial bleeding-associated factor**, **Left-right determination factor A**, **Lefty-A protein**  
 Gene name **Name: EBAF**  
 Synonyms: **LEFTA**, **LEFTYA**, **TGFB4**  
 From **Homo sapiens (Human)** [TaxID: [9606](#)]  
 Taxonomy **Eukaryota**; **Metazoa**; **Chordata**; **Craniata**; **Vertebrata**; **Euteleostomi**; **Mammalia**; **Eutheria**; **Primates**; **Catarrhini**; **Hominidae**; **Homo**.

#### References

##### [1] SEQUENCE FROM NUCLEIC ACID.

**TISSUE=Placenta;**  
 MEDLINE=97298127;PubMed=9153275 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]  
Kothapalli R., Buyukal I., Wu S.-Q., Chegini N., Tabibzadeh S.;  
 "Detection of eba, a novel human gene of the transforming growth factor beta superfamily association of gene expression with endometrial bleeding.";  
J. Clin. Invest. 99:2342-2350(1997).

##### [2] REVISIONS.

MEDLINE=99162193;PubMed=10053005 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]  
Kothapalli R.;  
 Unpublished results, cited by: Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G.,

Casey B.; Am. J. Hum. Genet. 64:712-721(1999).

[3] SEQUENCE FROM NUCLEIC ACID, AND VARIANT L-R AXIS MALFORMATIONS ASN-342.

**TISSUE=Placenta;**

MEDLINE=99162193;PubMed=10053005 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G., Casey B.;

"Characterization and mutation analysis of human LEFTY A and LEFTY B, homologues of murine genes implicated in left-right axis development.";

Am. J. Hum. Genet. 64:712-721(1999).

[4] SEQUENCE FROM NUCLEIC ACID.

DOI=[10.1038/ng1285](https://doi.org/10.1038/ng1285);PubMed=14702039 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., , Sugano S.;

"Complete sequencing and characterization of 21,243 full-length human cDNAs.";

Nat. Genet. 36:40-45(2004).

[5] SEQUENCE FROM NUCLEIC ACID.

**TISSUE=Ovary;**

DOI=[10.1073/pnas.242603899](https://doi.org/10.1073/pnas.242603899);MEDLINE=22388257;PubMed=12477932 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., , Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

## Comments

- **FUNCTION:** Required for left-right (L-R) asymmetry determination of organ systems in mammals. May play a role in endometrial bleeding.
- **SUBCELLULAR LOCATION:** Secreted.
- **TISSUE SPECIFICITY:** Mesenchymal cells of the endometrial stroma.
- **DEVELOPMENTAL STAGE:** Transiently expressed before and during menstrual bleeding.
- **PTM:** The processing of the protein may also occur at the second R-X-X-R site located at AA 132-135. Processing appears to be regulated in a cell-type specific manner.
- **DISEASE:** Defects in EBAF are the cause of left-right axis malformations (L-R axis malformation) [[MIM:601877](#)]. The defect includes left pulmonary isomerism, with cardiac anomalies characterized by complete atrioventricular canal defect and hypoplastic left ventricle, and interrupted inferior vena cava.
- **SIMILARITY:** Belongs to the TGF-beta family.

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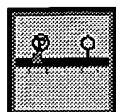
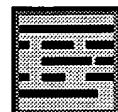
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	AF081511; AAC32600.1; - [ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
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CleanEx	<a href="#">HGNC:3122</a> ; EBAF.	
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GeneLynx	<a href="#">EBAF</a> ; Homo sapiens.	
GenAtlas	<a href="#">EBAF</a> .	
H-InvDB	<a href="#">HIX0001640</a> ; -.	
MIM	601877 <a href="#">[NCBI / EBI]</a> . <a href="#">GO:0007275</a> ; Biological process: development ( <i>traceable author statement</i> ). <a href="#">GO:0007309</a> ; Biological process: oocyte axis determination ( <i>traceable author statement</i> ).	
GO	<a href="#">GO:0007179</a> ; Biological process: transforming growth factor beta receptor signaling pathway ( <i>traceable author statement</i> ). <a href="#">QuickGo view</a> .	
SOURCE	<a href="#">EBAF</a> ; Homo sapiens.	
Ensembl	O00292; Homo sapiens. <a href="#">[Entry / Contig view]</a>	
	<a href="#">IPR001839</a> ; TGFb.	
InterPro	<a href="#">IPR001111</a> ; TGFb_N. <a href="#">Graphical view of domain structure</a> .	
Pfam	<a href="#">PF00019</a> ; TGF_beta; 1. <a href="#">PF00688</a> ; TGFb_propeptide; 1. <a href="#">Pfam graphical view of domain structure</a> .	
ProDom	<a href="#">PD000357</a> ; TGFb; 1. <a href="#">[Domain structure / List of seq. sharing at least 1 domain]</a>	
PROSITE	<a href="#">PS00250</a> ; TGF_BETA_1; 1.	
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DIP	<a href="#">O00292</a> .	
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SMR	<a href="#">O00292</a> ; 63A416CAE30F7A39.	
SWISS-2DPAGE	<a href="#">Get region on 2D PAGE</a> .	
UniRef	View cluster of proteins with at least <u>50%</u> / <u>90%</u> identity.	

**Keywords**

**Cytokine**; **Developmental protein**; **Disease mutation**; **Glycoprotein**; **Growth factor**; **Multigene family**; **Signal**.

**Features**

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Key	From	To	Length	Description	FTId
SIGNAL	1	21	21	Potential.	
PROPEP	22	76	55	Or 135 (Potential).	
CHAIN	77	366	290	Transforming growth factor beta 4.	
DISULFID	251	264	13	By similarity.	
DISULFID	263	316	53	By similarity.	
DISULFID	293	351	58	By similarity.	
DISULFID	297	353	56	By similarity.	
CARBOHYD	158	158	0	N-linked (GlcNAc...) (Potential).	
VARIANT	342	342	0	*	S -> N (in L-R axis malformations). <a href="#">VAR_010385</a>
CONFLICT	183	183	0	A -> P (in Ref. 4).	

**Sequence information**

Length: **366 AA** [This is the length of the unprocessed precursor]

Molecular weight: **40920 Da** [This is the MW of the unprocessed precursor]

CRC64: **63A416CAE30F7A39** [This is a checksum on the sequence]

10	20	30	40	50	60
MWPLWL	WVPLLAGPGA	ALTEEQ	LLRQLQLSEV	PVLDRADMEK	LVIPAHVRAQ
70	80	90	100	110	120
YVVLLRRSHG	DRSRGKRF	SFREVAGRFL	ASEASTHLLV	FGMEQLPPN	SELVQAVLRL
130	140	150	160	170	180
FQEPVPKAAL	HRHGRLSPRS	AQARVTVEWL	RVRDDGSNRT	SLIDSRLVSV	HESGWKAFDV
190	200	210	220	230	240
TEAVNFWQQL	SRPRQPLLQ	VSVQREHLGP	LASGAHKLVR	FASQGAPAGL	GEPQLELHTL
250	260	270	280	290	300
DLRDYGAQGD	CDPEAPMTEG	TRCCRQEMYI	DLQGMKWAKN	WVLEPPGFLA	YECVGTCQQP
310	320	330	340	350	360
PEALAFNWPF	LGPRQCIASE	TASLPMIVSI	KEGGRTRPQV	VSLPNMRVQK	CSCASDGALV

PRRLQP

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**Multiple forms of TGF-beta: distinct promoters and differential expression.**

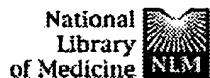
Roberts AB, Kim SJ, Noma T, Glick AB, Lafyatis R, Jakowlew SB, Geiser A, O'Reilly MA, Danielpour D,

Laboratory of Chemoprevention, National Cancer Institute, Bethesda, MD 20892.

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There are now five known distinct isoforms of TGF-beta. Of these, only TGF-beta 1, 2 and 3 thus far have been demonstrated to be expressed in mammalian tissues; TGF-beta 4 has been described only in chicken and TGF-beta 5 only in feline. The biological activities of these five isoforms of TGF-beta are indistinguishable in most in vitro assays, although their sites of synthesis and localization in vivo are often distinct. Expression of the isoforms is differentially controlled both in vivo, as in development and in vitro after treatment of cells with steroids, such as tamoxifen, or with retinoids. To investigate the basis for these observations we have cloned and characterized the promoters of the human TGF-beta 1, 2 and 3 genes. Significant differences were found: whereas the TGF-beta 1 promoter has no TATAAA sequence, it is regulated principally by AP-1 sites, both the TGF-beta 2 and 3 promoters have TATAAA boxes as well as AP-2 sites and

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**Transforming growth factor beta 1 expression in the endometrium of the mare during placentation.****Lennard SN, Stewart F, Allen WR.**

Thoroughbred Breeders' Association Equine Fertility Unit, Paddocks, Suffolk, United Kingdom.

PubMed Services

In situ hybridization, Northern blotting, and immunohistochemical techniques were used to study the expression of transforming growth factor beta 1 (TGF beta 1) in the endometrium of the mare during the first 150 days of pregnancy (term = 330-340 days). In situ hybridization using an oligonucleotide (45mer) probe, based on a homologous region within all known mammalian TGF beta 1 sequences, demonstrated TGF beta 1 mRNA accumulation in the glandular and luminal epithelial cells of the endometrium from day 10 onwards which corresponds to the time of implantation. Expression in the endometrium remained at a high level throughout the sampling period (day 150). There was also marked expression of TGF beta 1 in the mononuclear cells accumulated around the specialized trophoblast cells of the endometrial stroma. Endometrial stroma of mares carrying failing donkey-in-pregnancies created by embryo transfer. The sense (complementary) oligonucleotide probe exhibited no hybridization to any

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stage. Northern blot analysis demonstrated that the oligonucleotide probe and a porcine TGF beta 1 cDNA clone hybridized to a 1.5 kb transcript in horse endometrial and lymphocyte RNA validating the oligonucleotide probe for detection of horse mRNA. Furthermore, both probes demonstrated an increase in the pregnant endometrium from day 33 onwards, thereby supporting the in situ hybridization results. Immunostaining with a rabbit anti-bovine TGF beta 1 serum also showed increasing TGF beta 1 accumulation in endometrial epithelia during pregnancy, of the protein in endometrial stroma and in the trophoblast after day 60 of pregnancy. These results suggest that TGF beta 1 expression increases in the maternal endometrium at the time of implantation and that it may play a role in endometrial and/or trophoblast growth and differentiation during placentation in this species. It may also influence fetal (via placental transfer) at a later stage of gestation.

PMID: 8562058 [PubMed - indexed for MEDLINE]

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- Nature. 1996 May 9;381(6578):116-7.
- Nature. 1997 Jan 9;385(6612):111-2.

**Left-right asymmetric expression of the TGF member lefty in mouse embryos.**

Meno C, Saijoh Y, Fujii H, Ikeda M, Yokoyama T, Y Toyoda Y, Hamada H.

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Tokyo Metropolitan Institute of Medical Science, Japan

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Examples of lateral asymmetry are often found in vertebrates, such as the heart being on the left side, but the molecular mechanisms governing the establishment of this left-right (L-R) axis are unknown. A diffusible morphogen may determine L-R polarity, but the likely molecule has not so far been identified. Here we report the cloning of a gene, lefty, a member of the transforming growth factor- $\beta$  superfamily. lefty encodes a protein which may encode a morphogen for L-R determination. The gene contains the cysteine-knot motif characteristic of this family and is secreted as a processed form of relative molecular mass 25K-32K. Surprisingly, lefty is expressed in the left half of the gastrulating mouse embryo. This asymmetric expression is transient and occurs just before the first sign of lateralization appears. In the mouse mutants iv and inv, which cause s

the sites of lefty expression are inverted, indicating th downstream of iv and inv. These results suggest that lef involved in setting up L-R asymmetry in the organ system

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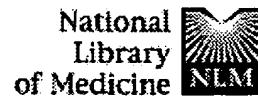
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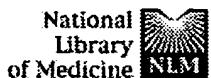
## **Transforming growth factor beta 1 expression in the endometrium of the mare during placentation.**

**Lennard SN, Stewart F, Allen WR.**

Thoroughbred Breeders' Association Equine Fertility Unit, Mertoun Paddock, United Kingdom.

In situ hybridization, Northern blotting, and immunohistochemical technique study the expression of transforming growth factor beta 1 (TGF beta 1) in the endometrium of the mare during the first 150 days of pregnancy (term = 330-340 days). In situ hybridization using an oligonucleotide (45mer) probe, based on a homologous sequence within all known mammalian TGF beta 1 DNA sequences, demonstrated TGF beta 1 mRNA accumulation in the glandular and luminal epithelial cells of the endometrium from day 33 onwards which corresponds to the time of implantation (day 33). Expression in the endometrium remained at a high level to the end of the second trimester (day 150). There was also marked expression of TGF beta 1 in the mononuclear cells accumulated around the periphery of the specialized trophoblast cells of the conceptus within the endometrium and in the mononuclear cells accumulated in the stroma of mares carrying failing donkey-in-horse pregnancies created by embryo transfer. The sense (control) oligonucleotide probe exhibited no hybridization to any tissue stage. Northern blot analysis demonstrated that the oligonucleotide probe and the TGF beta 1 cDNA clone hybridized to a single 2.5 kb transcript in horse endometrial lymphocyte RNA, thus validating the oligonucleotide probe for detection of TGF beta 1 mRNA. Furthermore, both probes demonstrated an increased signal in the endometrium from day 33 onwards, thereby confirming the in situ hybridization results. Immunostaining with a specific anti-bovine TGF beta 1 serum also showed increased TGF beta 1 accumulation in endometrial epithelia during pregnancy, and localized the protein in endometrial stroma and in the trophoblast layer of the placenta at the time of implantation. These results show that TGF beta 1 expression increases in the endometrium of the mare at the time of implantation and that it may play a role in regulating endometrial and/or trophoblast growth and differentiation during this species. It may also influence fetal development (via placental transfer) at this stage of gestation.

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**Cytokine expression in human endometrium thr menstrual cycle.**

Tabibzadeh S, Sun XZ.

Department of Pathology, University of South Florida H Center, Tampa 33612.

PubMed Services

Recent evidence suggests that diverse endometrial func regulated by cytokines. In this report, the presence of mRNA of cytokines were studied in human endometrium the menstrual cycle. The presence of the interleukin-1 (interleukin-1 (IL-1) beta, interleukin receptor antagonis interleukin-6 (IL-6) and transforming growth factor (TG proteins were demonstrated by immunohistochemical st IL-1 alpha and TGF-alpha proteins were strongly expres beta protein was weakly expressed in all the cells in the as epithelial cells. IRAP was markedly expressed in the morphological features of macrophages scattered in the the expression of IL-6 protein was predominant in the e epithelium. Diffuse cytoplasmic expression of IL-1 alpha endometrial epithelium during the proliferative phase co markedly with its enhanced luminal expression during th phase of the menstrual cycle. In addition, the presence of these cytokines in endometrium was established thro

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entire menstrual cycle by reverse transcription-polymer reaction (RT-PCR). Abundant expression of cytokines in endometrium emphasizes the significant roles that cyto cell-cell interactions and in regulating endometrial funct

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09393628 PMID: 1353860

Correction: a new interpretation of a chicken transforming growth factor-beta 4 complementary DNA.

Burt D W ; Jakowlew S B

Department of Cellular and Molecular Biology, Edinburgh Research Station, Roslin, Midlothian, United Kingdom.

Molecular endocrinology (Baltimore, Md.) (UNITED STATES) Jun 1992 ,

6 (6) p989-92, ISSN 0888-8809 Journal Code: 8801431

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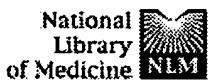
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Molecular Sequence Databank No.: GENBANK/X08012

CAS Registry No.: 0 (Protein Precursors); 0 (Protein Sorting Signals); 0 (Transforming Growth Factor beta); 110343-45-8 (transforming growth factor beta precursor); 9007-49-2 (DNA)

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**Immunochemical study of transforming growth in the kidney of the rat and chicken.**

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**Diaz-Ruiz C, Montaner B, Perez-Tomas R.**Department de Biologia Cellular i Anatomia Putologica, L  
(Barcelona), Spain.

PubMed Services

Transforming growth factor-beta (TGF-beta) is a homo polypeptide of 25 kDa, which regulates cell growth and influences extracellular matrix metabolism. Using im techniques, we identified TGF-beta in the loops of Henle collecting and Bellini ducts of rat kidney and in the loop chicken kidney. Furthermore, we detected two TGF-beta-immunoreactive proteins on kidney blots of th and 47 kDa, and three on chicken kidney blots of 12.5, 3 We suggest that the precursor forms of rat and chick or beta 3, chicken TGF-beta 4, and the mature form of expressed in the collecting and Bellini ducts of rat kidne loops of Henle of rat and chicken kidney.

PMID: 8791107 [PubMed - indexed for MEDLINE]

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1: Mol Endocrinol. 1992 Jun;6(6):989-92.

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**Correction: a new interpretation of a chicken growth factor-beta 4 complementary DNA.**

Burt DW, Jakowlew SB.

Department of Cellular and Molecular Biology, Edinburgh Station, Roslin, Midlothian, United Kingdom.

PMID: 1353860 [PubMed - indexed for MEDLINE]

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L3: Entry 1 of 8

File: USPT

Nov 18, 2003

US-PAT-NO: 6649588

DOCUMENT-IDENTIFIER: US 6649588 B1

TITLE: Inhibition of TGF-.beta. and uses thereof

DATE-ISSUED: November 18, 2003

US-CL-CURRENT: 514/2; 514/21, 514/899, 530/350

INT-CL: [07] A61 K 38/00, A01 N 25/00, C07 K 17/00

1, 14, 15  
- abnormal bleeding  
- uterine bleeding  
- menstrual bleeding

L3: Entry 2 of 8

File: USPT

Aug 6, 2002

US-PAT-NO: 6428966

DOCUMENT-IDENTIFIER: US 6428966 B1

\*\* See image for Certificate of Correction \*\*

TITLE: Growth differentiation factor, lefty-1

DATE-ISSUED: August 6, 2002

US-CL-CURRENT: 435/7.1, 435/252.3, 435/254.11, 435/320.1, 435/325, 435/7.7,  
435/7.9, 530/350, 530/351, 530/387.1, 530/387.9, 530/388.1, 530/388.23, 530/388.24,  
530/389.1, 530/389.2, 536/23.1, 536/23.5

INT-CL: [07] C07 K 14/475, C12 N 1/21, C12 N 5/10, C12 N 15/19, C12 N 15/63

L3: Entry 3 of 8

File: USPT

Sep 25, 2001

US-PAT-NO: 6294662

DOCUMENT-IDENTIFIER: US 6294662 B1

TITLE: Nucleic acids encoding an endometrial bleeding associated factor (ebaf)

DATE-ISSUED: September 25, 2001

US-CL-CURRENT: 536/23.5; 435/6, 536/23.1, 536/24.31, 536/24.33

INT-CL: [07] C07 H 21/04, C12 Q 1/68

L3: Entry 4 of 8

File: USPT

Jun 29, 1999

US-PAT-NO: 5916751

DOCUMENT-IDENTIFIER: US 5916751 A

TITLE: Method for the diagnosis of selected adenocarcinomas

DATE-ISSUED: June 29, 1999

US-CL-CURRENT: 435/6; 435/7.23, 436/64, 436/813

INT-CL: [06] G01 N 33/574, G01 N 33/48, C12 Q 1/68

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L3: Entry 5 of 8

File: DWPI

Nov 18, 2003

DERWENT-ACC-NO: 2002-352240

ABSTRACTED-PUB-NO: WO 200229105A

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TITLE: Inhibiting the activity of transforming growth factor (TGF) beta, for treating e.g. fibrosis, comprises contacting tissue expressing TGF beta with ebaF peptide its analogue

INT-CL (IPC): A01 N 25/00, A01 N 37/18, A61 K 38/00, C07 K 1/00, C07 K 14/00, C07 K 17/00, C12 Q 1/68, G01 N 33/574

Derwent-CL (DC): B01, B04, B05, D16

CPI Codes: B04-E03F; B04-E08; B04-F11; B04-H06F; B04-N02; B14-F01; B14-F08; B14-G02D; B14-H01; B14-J05E; B14-L06; B14-N12; B14-N14; B14-N17A; B14-N17B; B14-S03; D05-H12A; D05-H12E; D05-H12F;

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L3: Entry 6 of 8

File: DWPI

Sep 25, 2001

DERWENT-ACC-NO: 2001-647266

ABSTRACTED-PUB-NO: US 6294662B

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TITLE: New nucleic acid molecule encoding endometrial bleeding associated factor, useful in early diagnosis of selected adenocarcinomas in human, e.g. adenocarcinomas of colon, ovaries or testis

INT-CL (IPC): C07 H 21/04, C12 Q 1/68

Derwent-CL (DC): B04, D16

CPI Codes: B04-E03F; B04-E05; B11-C08E5; B12-K04A1; D05-H09; D05-H12A; D05-H12D1;

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L3: Entry 7 of 8

File: DWPI

Jun 29, 1999

DERWENT-ACC-NO: 1999-384717

ABSTRACTED-PUB-NO: US 5916751A

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TITLE: Detecting serous or mucinous colon/ovarian adenocarcinomas and testicular adenocarcinoma by assaying for elevated expression of a gene

INT-CL (IPC): C12 Q 1/68, G01 N 33/48, G01 N 33/574

Derwent-CL (DC): B04, D16, S03

CPI Codes: B04-B04C2; B04-B04L; B04-E01; B04-E05; B04-G02; B04-G21; B04-H01; B11-C07A; B11-C08E5; B12-K04A1; B12-K04F; D05-H09;

EPI Codes: S03-E14H1; S03-E14H4; S03-E14H6;

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L3: Entry 8 of 8

File: DWPI

Jan 30, 2003

DERWENT-ACC-NO: 1999-153704

ABSTRACTED-PUB-NO: US 6428966B

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L9: Entry 1 of 2

File: USPT

Aug 6, 2002

US-PAT-NO: 6428966DOCUMENT-IDENTIFIER: US 6428966 B1**\*\* See image for Certificate of Correction \*\***

TITLE: Growth differentiation factor, lefty-1

DATE-ISSUED: August 6, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lee; Se-Jin	Baltimore	MD		
Huynh; Thanh	Baltimore	MD		
Sebald; Suzanne	Jessup	MD		

## ASSIGNEE-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY	TYPE	CODE
The Johns Hopkins University School of Medicine	Baltimore	MD			02	

APPL-NO: 09/ 485053 [PALM]

DATE FILED: January 31, 2000

## PARENT-CASE:

This application is an application filed under 35 U.S.C. 371 from PCT/US98/15352, filed Jul. 24, 1998 which claims benefit from U.S. Provisional application 60/054,382 filed Jul. 31, 1997, both of which are incorporated by reference in their entirety.

## PCT-DATA:

APPL-NO	DATE-FILED	PUB-NO	PUB-DATE	371-DATE	102(E)-DATE
PCT/US98/15352	July 24, 1998	WO99/06444	Feb 11, 1999	Mar 5, 2000	Mar 5, 2000

INT-CL: [07] C07 K 14/475, C12 N 1/21, C12 N 5/10, C12 N 15/19, C12 N 15/63

US-CL-ISSUED: 435/7.1, 435/7.7, 435/7.9, 435/320.1, 435/325, 435/252.3, 435/254.11, 530/350, 530/351, 530/387.1, 530/387.9, 530/388.1, 530/388.23, 530/388.24, 530/389.1, 530/389.2, 536/23.1, 536/23.5

US-CL-CURRENT: 435/7.1; 435/252.3, 435/254.11, 435/320.1, 435/325, 435/7.7, 435/7.9, 530/350, 530/351, 530/387.1, 530/387.9, 530/388.1, 530/388.23, 530/388.24, 530/389.1, 530/389.2, 536/23.1, 536/23.5

FIELD-OF-SEARCH: 536/23.1, 536/23.5, 435/320.1, 435/325, 435/252.3, 435/7.1, 435/7.7, 435/7.9, 435/254.11, 530/387.1, 530/350, 530/387.9, 530/388.1, 530/388.23, 530/254.11, 530/388.24, 530/389.1, 530/389.2, 530/351

## PRIOR-ART-DISCLOSED:

## U.S. PATENT DOCUMENTS

PAT-NO	ISSUE-DATE	PATENTEE-NAME	US-CL
<input type="checkbox"/> <u>5194596</u>	March 1993	Tischer et al.	
<input type="checkbox"/> <u>5350836</u>	September 1994	Kopchick et al.	
<input type="checkbox"/> <u>6027917</u>	February 2000	Celeste et al.	

## OTHER PUBLICATIONS

Vukicevic et al., 1996, PNAS USA 93:9021-9026.\*  
Massague, 1987, Cell 49:437-438.\*  
Pilbeam et al., 1993, Bone 14:717-720.\*  
Benjamin et al., 1998, Development 125:1591-1598.\*  
Skolnick et al., 2000, Trends in Biotech. 18:34-39.\*  
Bork, 2000, Genome Research 10:398-4000.\*  
Doerks et al., 1998, Trends in Genetics 14:248-250.\*  
Smith et al., 1997, Nature Biotechnology 15:1222-1223.\*  
Brenner, 1999, Trends in Genetics 15:132-133.\*  
Bork et al., 1996, Trends in Genetics 12:425-427.\*  
Wells, 1990, Biochemistry 29:8509-8517.\*  
Ngo et al., 1994, The Protein Folding Problem and Tertiary Structure Prediction,  
Merz et al., eds., Birkhauser, Boston, pp. 492-495.\*  
Lyons and Moses. "Transforming Growth Factors and Regulation of Cell Proliferation,"  
Proliferation," Eur. J. Biochem, 187:467-473 (1990), FEBS.  
Massague . "The TGF-.beta. Family of Growth and Differentiation Factors," Cell,  
49:437-438 (1987), Cell Press.  
McDonald and Hendrickson. "A Structural Superfamily of Growth Factors Containing a  
Cystine Knot Motif," Cell, 73:421-424 (1993), Cell Press.  
Sporn and Roberts. "Transforming Growth Factor-beta: New Chemical Forms and New  
Biological Roles," BioFactors, 1(1):89-93 (1988), IRL Press.  
Beddington, Rosa, "Left, Right, Left . . . Turn," Nature 381:116-117, 1996.  
Kosaki, K., et al., "Characterization and Mutation Analysis of Human LEFTY A and  
LEFTY B, Homologues of Murine Genes Implicated in Left-Right Axis Development," Am.  
J. Hum. Genet. 64:712-721, 1999.  
Kothapalli, Ravi et al., "Detection of ebaf, a Novel Human Gene of the Transforming  
Growth Factor .beta..Superfamily," J. Clin. Invest. 99:(10)2342-2350, 1997.  
Meno, Chikara et al., "Left-Right Asymmetric Expression of the TGF.beta.-Family  
Member lefty in Mouse Embryos," Nature 381:151-155, 1996.  
Meno, Chikara et al., "Lefty-1 Is Required for Left-Right Determination as a  
Regulator of lefty-2 and nodal," Cell 94:287-297, 1998..  
Schlange, Thomas et al., "Chick CFC Controls Lefty1 Expression in the Embryonic  
Midline and Nodal Expression in the Lateral Plate," Developmental Biology 234:376-  
389, 2001.  
Yoshioka, Hidefumi et al., "Pitx2, a Bicoid-Type Homeobox Gene, Is Involved in a  
Lefty-Signaling Pathway in Determination to Left-Right Asymmetry," Cell 94:299-305,  
1998.

ART-UNIT: 1646

PRIMARY-EXAMINER: Kemmerer; Elizabeth

ATTY-AGENT-FIRM: Gary Cary Ware &amp; Freidenrich LLP Haile; Lisa A.

**ABSTRACT:**

Growth differentiation factor Lefty-1 polypeptide and polynucleotides are provided herein. Also disclosed are diagnostic and therapeutic methods of using the Lefty-1 polypeptide and polynucleotide sequences.

22 Claims, 1 Drawing figures

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	<u>#1</u> Search 1992 endocrinology burt	09:48:02	<u>0</u>

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**Search Results - Record(s) 1 through 2 of 2 returned.**

L2: Entry 1 of 2

File: USPT

Jan 27, 2004

US-PAT-NO: 6683156

DOCUMENT-IDENTIFIER: US 6683156 B1

\*\* See image for Certificate of Correction \*\*

TITLE: Method for diagnosing selected adenocarcinomas

DATE-ISSUED: January 27, 2004

US-CL-CURRENT: 530/350; 530/351, 530/399, 536/23.1, 536/23.5INT-CL: [07] C07 K 17/00, C07 H 21/04

L2: Entry 2 of 2

File: DWPI

Jan 27, 2004

DERWENT-ACC-NO: 2004-118581

ABSTRACTED-PUB-NO: US 6683156B

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TITLE: New endometrial bleeding associated factor protein, useful for diagnosing a mucinous adenocarcinoma of the ovaries or colon in a female human or of the testis or colon of a male human

INT-CL (IPC): C07 H 21/04, C07 K 17/00

Derwent-CL (DC): B04, D16

CPI Codes: B04-C01G; B04-E03F; B04-N02A0E; B11-C08F4; B12-K04A1; D05-H09; D05-H12A;

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TITLE: A new growth differentiation factor, Lefty-1 - useful to detect and treat cell proliferative and immunological disorders

INT-CL (IPC): A61 K 38/18, C07 K 14/475, C07 K 16/22, C12 N 1/21, C12 N 5/06, C12 N 5/10, C12 N 15/12, C12 N 15/19, C12 N 15/63, C12 P 21/02, G01 N 33/48, G01 N 33/53

Derwent-CL (DC): B04, D16, S03

CPI Codes: B04-C01; B04-E08; B04-F0100E; B04-G02; B04-H06; B12-K04A1; B12-K04A3; B14-G03; B14-H01; B14-H01B; B14-N17A; B14-P01; D05-H09; D05-H11; D05-H12A; D05-H12E; D05-H14; D05-H17A2;

EPI Codes: S03-E14H; S03-E14H4;

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NCBI BLAST program reference [PMID:[9254694](#)]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query length: 366 AA (of which 8% low-complexity regions filtered out)

Date run: 2004-11-09 10:42:40 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProt

1,621,919 sequences; 518,174,383 total letters

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Db	AC	Description	Score	E-value
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<input type="checkbox"/>	<a href="#">sp_075610</a>	LFTB_HUMAN Left-right determination factor B precursor...	<u>654</u>	0.0
<input type="checkbox"/>	<a href="#">tr_Q8BMF7</a>	Mus musculus 13 days embryo male testis cDNA, RIKEN fu...	<u>567</u>	e-160
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<input type="checkbox"/>	<a href="#">sp_Q64280</a>	TGF4_MOUSE Transforming growth factor beta 4 precursor...	<u>556</u>	e-157
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<input type="checkbox"/>	<a href="#">tr_Q9DD36</a>	Xantivin (Lefty-related factor Xatv) [Xantivin] [Xenop...	<u>229</u>	8e-59
<input type="checkbox"/>	<a href="#">tr_Q9DFC5</a>	TGF-beta family member lefty-B [Xenopus laevis (Africa...	<u>228</u>	1e-58
<input type="checkbox"/>	<a href="#">tr_Q9PVN4</a>	Lefty [Gallus gallus (Chicken)]	<u>226</u>	7e-58
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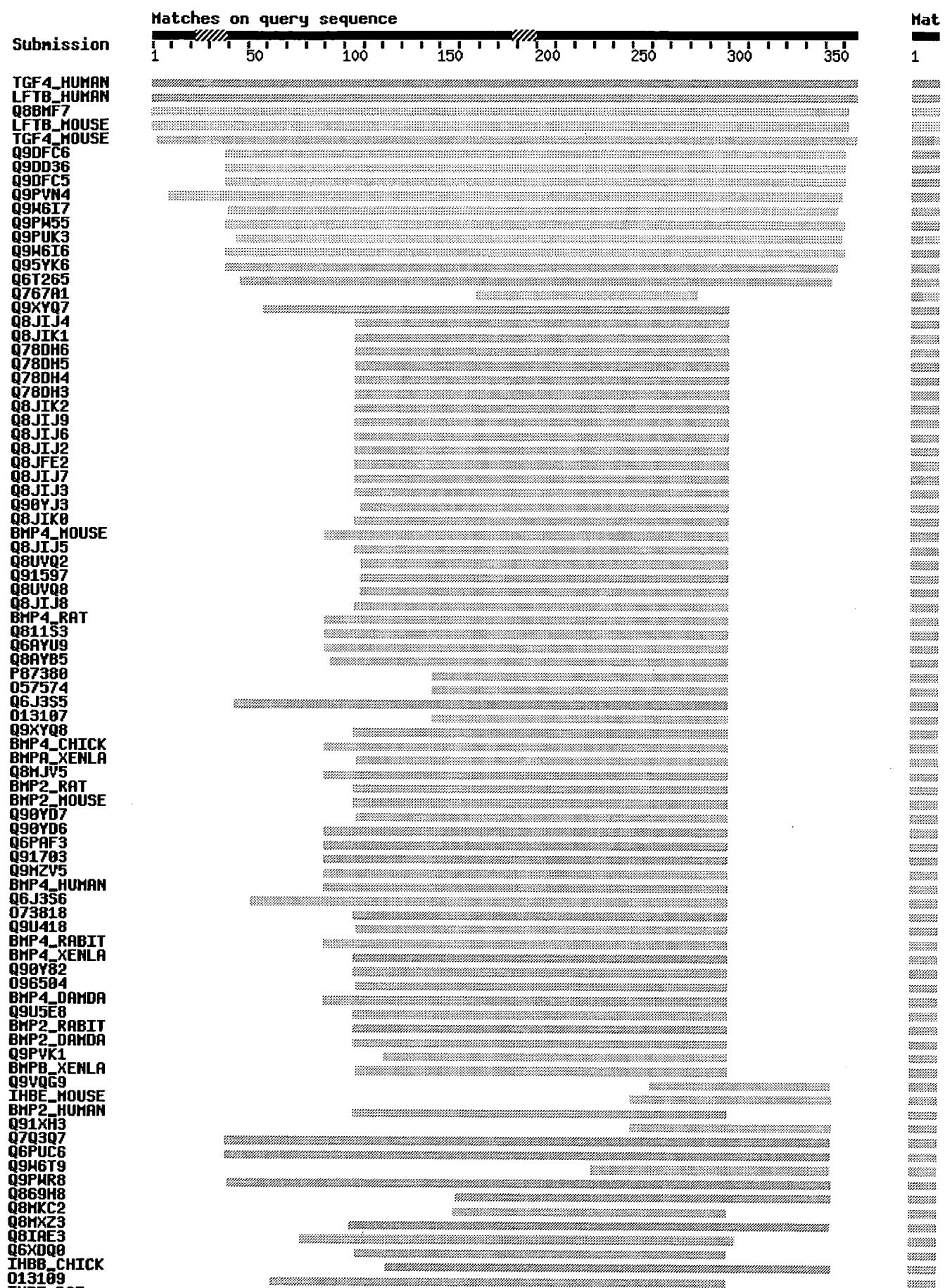
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<input type="checkbox"/>	tr	<a href="#">Q90YJ3</a>	Anti-dorsalizing morphogenetic protein [admp]	[Brachydanio rerio (Zebrafish) (Danio rerio)]	65	2e-09	
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<input type="checkbox"/>	tr	<a href="#">Q8JIJ5</a>	Bmp4 protein [Bmp4]	[Oreochromis niloticus (Nile tilapia)]	64	3e-09	
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<input type="checkbox"/>	tr	<a href="#">Q811S3</a>	Bone morphogenetic protein 4 [Bmp4]	[Rattus norvegicus]	63	1e-08	
<input type="checkbox"/>	tr	<a href="#">Q6AYU9</a>	Bmp4 protein [Bmp4]	[Rattus norvegicus (Rat)]	63	1e-08	
<input type="checkbox"/>	tr	<a href="#">Q8AYB5</a>	Bone morphogenetic protein 4 (Fragment)	[Oryzias latipes]	62	2e-08	
<input type="checkbox"/>	tr	<a href="#">P87380</a>	Bone morphogenetic protein-4 (Fragment)	[bmp4]	[Brachydanio rerio (Zebrafish) (Danio rerio)]	62	2e-08
<input type="checkbox"/>	tr	<a href="#">O57574</a>	Bone genetic protein 4 (Hypothetical protein)	(Bone morphogenetic protein 4)	62	2e-08	
<input type="checkbox"/>	tr	<a href="#">Q6J3S5</a>	Bone morphogenetic protein 24B [BMP24B]	[Petromyzon marinus]	61	3e-08	
<input type="checkbox"/>	tr	<a href="#">O13107</a>	BMP4 [bmp4]	[Brachydanio rerio (Zebrafish) (Danio rerio)]	61	4e-08	
<input type="checkbox"/>	tr	<a href="#">Q9XYQ8</a>	Bone morphogenetic protein BMP2/4 (Fragment)	[BMP2/4]	61	4e-08	
<input type="checkbox"/>	sp	<a href="#">Q90752</a>	BMP4_CHICK	Bone morphogenetic protein 4 precursor (BMP-4)	60	5e-08	
<input type="checkbox"/>	sp	<a href="#">P25703</a>	BMPA_XENLA	Bone morphogenetic protein 2-I precursor (BMP-2)	59	1e-07	
<input type="checkbox"/>	tr	<a href="#">Q8MJV5</a>	Bone morphogenetic protein 4 [sBmp4]	[Suncus murinus]	59	2e-07	
<input type="checkbox"/>	sp	<a href="#">P49001</a>	BMP2_RAT	Bone morphogenetic protein 2 precursor (BMP-2)	57	4e-07	
<input type="checkbox"/>	sp	<a href="#">P21274</a>	BMP2_MOUSE	Bone morphogenetic protein 2 precursor (BMP-2)	57	4e-07	
<input type="checkbox"/>	tr	<a href="#">Q90YD7</a>	Bone morphogenetic protein 2 (BMP-2)	[BMP-2]	[Xenopus tropicalis]	57	4e-07
<input type="checkbox"/>	tr	<a href="#">Q90YD6</a>	Bone morphogenetic protein 4 [BMP-4]	[Xenopus tropicalis]	57	4e-07	
<input type="checkbox"/>	tr	<a href="#">Q6PAF3</a>	LOC397874 protein [LOC397874]	[Xenopus laevis (African clawed frog)]	57	7e-07	

<input type="checkbox"/>	tr	<u>Q91703</u>	Bone morphogenetic protein 4 [BMP-4]	[Xenopus laevis (...)	<u>57</u>	7e-07
<input type="checkbox"/>	tr	<u>Q9MZV5</u>	Bone morphogenetic protein 4 (Fragment)	[bmp4] [Canis ...	<u>57</u>	7e-07
<input type="checkbox"/>	sp	<u>P12644</u>	BMP4_HUMAN	Bone morphogenetic protein 4 precursor (BMP...	<u>56</u>	9e-07
<input type="checkbox"/>	tr	<u>Q6J3S6</u>	Bone morphogenetic protein 24A [BMP24A]	[Petromyzon ma...	<u>56</u>	9e-07
<input type="checkbox"/>	tr	<u>Q73818</u>	Bone morphogenetic protein 4 [BMP-4]	[Xenopus laevis (...)	<u>56</u>	9e-07
<input type="checkbox"/>	tr	<u>Q9U418</u>	Bone morphogenetic protein 2/4 [BMP2/4]	[Branchiostoma...	<u>56</u>	1e-06
<input type="checkbox"/>	sp	<u>Q46576</u>	BMP4_RABIT	Bone morphogenetic protein 4 precursor (BMP...	<u>55</u>	2e-06
<input type="checkbox"/>	sp	<u>P30885</u>	BMP4_XENLA	Bone morphogenetic protein 4 precursor (BMP...	<u>55</u>	2e-06
<input type="checkbox"/>	tr	<u>Q90Y82</u>	LjBmp2/4a (Fragment)	[LjBmp2/4a] [Lampetra japonica (J...]	<u>55</u>	2e-06
<input type="checkbox"/>	tr	<u>Q96504</u>	Bone morphogenetic protein 2/4 [AmphiBMP2/4]	[Branchio...	<u>55</u>	2e-06
<input type="checkbox"/>	sp	<u>Q29607</u>	BMP4_DAMDA	Bone morphogenetic protein 4 precursor (BMP...	<u>54</u>	3e-06
<input type="checkbox"/>	tr	<u>Q9U5E8</u>	Pf-BMP2/4 [Pf-bmp2/4]	[Ptychodera flava]	<u>54</u>	3e-06
<input type="checkbox"/>	sp	<u>Q46564</u>	BMP2_RABIT	Bone morphogenetic protein 2 precursor (BMP...	<u>54</u>	4e-06
<input type="checkbox"/>	sp	<u>Q19006</u>	BMP2_DAMDA	Bone morphogenetic protein 2 precursor (BMP...	<u>54</u>	4e-06
<input type="checkbox"/>	tr	<u>Q9PVK1</u>	Anti-dorsalizing morphogenetic protein [ADMP]	[Gallus ...]	<u>54</u>	4e-06
<input type="checkbox"/>	sp	<u>P30884</u>	BMPB_XENLA	Bone morphogenetic protein 2-II precursor (...)	<u>53</u>	8e-06
<input type="checkbox"/>	tr	<u>Q9VQG9</u>	CG16987-PA (Cg16987-pb) (GH14433p)	[Alp23B] [Drosophil...	<u>53</u>	8e-06
<input type="checkbox"/>	sp	<u>Q08717</u>	IHBE_MOUSE	Inhibin beta E chain precursor (Activin bet...	<u>53</u>	1e-05
<input type="checkbox"/>	sp	<u>P12643</u>	BMP2_HUMAN	Bone morphogenetic protein 2 precursor (BMP...	<u>53</u>	1e-05
<input type="checkbox"/>	tr	<u>Q91XH3</u>	Inhibin beta E [Inhbe]	[Mus musculus (Mouse)]	<u>53</u>	1e-05
<input type="checkbox"/>	tr	<u>Q7Q3Q7</u>	AgCP11289 (Fragment)	[agCG50272] [Anopheles gambiae st...]	<u>53</u>	1e-05
<input type="checkbox"/>	tr	<u>Q6PUC6</u>	Decapentaplegic (Fragment)	[Anopheles gambiae (African...]	<u>53</u>	1e-05
<input type="checkbox"/>	tr	<u>Q9W6T9</u>	Activin beta B protein (Fragment)	[inhbb] [Brachydanio...]	<u>52</u>	2e-05
<input type="checkbox"/>	tr	<u>Q9PWR8</u>	Activin beta B subunit precursor	[Carassius auratus (G...]	<u>52</u>	2e-05
<input type="checkbox"/>	tr	<u>Q869H8</u>	GDF2 precursor	[Crassostrea gigas (Pacific oyster)]	<u>52</u>	2e-05
<input type="checkbox"/>	tr	<u>Q8MKC2</u>	Bone morphogenetic protein 2 (Fragment)	[Ovis aries (S...]	<u>52</u>	2e-05
<input type="checkbox"/>	tr	<u>Q8MXZ3</u>	Bone morphogenetic protein [HpBMP]	[Hemicentrotus pulc...]	<u>52</u>	2e-05
<input type="checkbox"/>	tr	<u>Q8IAE3</u>	Sj-BMP2/4 [Sj-bmp2/4]	[Stichopus japonicus (Sea cucumb...]	<u>51</u>	3e-05
<input type="checkbox"/>	tr	<u>Q6XDQ0</u>	Bone morphogenetic protein 2	[Gallus gallus (Chicken)]	<u>50</u>	5e-05
<input type="checkbox"/>	sp	<u>P27093</u>	IHBB_CHICK	Inhibin beta B chain precursor (Activin bet...)	<u>50</u>	6e-05
<input type="checkbox"/>	tr	<u>Q13109</u>	BMP2 [bmp2a]	[Brachydanio rerio (Zebrafish) (Danio rer...]	<u>50</u>	6e-05
<input type="checkbox"/>	sp	<u>Q88959</u>	IHBE_RAT	Inhibin beta E chain precursor (Activin beta-...)	<u>50</u>	8e-05
<input type="checkbox"/>	sp	<u>P17491</u>	IHBB_RAT	Inhibin beta B chain precursor (Activin beta-...)	<u>50</u>	8e-05
<input type="checkbox"/>	sp	<u>Q04999</u>	IHBB_MOUSE	Inhibin beta B chain precursor (Activin bet...)	<u>50</u>	8e-05
<input type="checkbox"/>	sp	<u>Q95393</u>	BM10_HUMAN	Bone morphogenetic protein 10 precursor (BM...	<u>50</u>	8e-05
<input type="checkbox"/>	sp	<u>P48969</u>	DVR1_STRPU	DVR-1 protein homolog precursor [DVR1] [Str...	<u>49</u>	1e-04
<input type="checkbox"/>	tr	<u>Q90261</u>	Activin beta B [inhbb]	[Brachydanio rerio (Zebrafish) ...]	<u>49</u>	1e-04
<input type="checkbox"/>	tr	<u>Q869H7</u>	GDF3 precursor (Fragment)	[Crassostrea gigas (Pacific ...]	<u>49</u>	1e-04
<input type="checkbox"/>	sp	<u>P09529</u>	IHBB_HUMAN	Inhibin beta B chain precursor (Activin bet...)	<u>49</u>	2e-04
<input type="checkbox"/>	tr	<u>Q9PTF9</u>	Bone morphogenetic protein 7 [bmp7]	[Brachydanio rerio...]	<u>49</u>	2e-04
<input type="checkbox"/>	tr	<u>Q6EH35</u>	Bone morphogenetic protein 2 (Fragment)	[BMP-2] [Trach...]	<u>49</u>	2e-04
<input type="checkbox"/>	sp	<u>P58166</u>	IHBE_HUMAN	Inhibin beta E chain precursor (Activin bet...)	<u>48</u>	2e-04
<input type="checkbox"/>	sp	<u>Q9R229</u>	BM10_MOUSE	Bone morphogenetic protein 10 precursor (BM...	<u>48</u>	2e-04
<input type="checkbox"/>	sp	<u>Q24735</u>	60A_DROVI	60A protein precursor (Glass bottom boat pro...)	<u>48</u>	2e-04
<input type="checkbox"/>	tr	<u>Q9DGF1</u>	Inhibin/activin (Fragment)	[Cyprinus carpio (Common ca...]	<u>48</u>	2e-04

**Graphical overview of the alignments**

**Click here** to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs  
( [Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

**Profile hits****Pfam hits**[TGFb\\_propeptide](#)[TGF\\_beta](#)



**Alignments**

sp O00292 Transforming growth factor beta 4 precursor (TGF-beta 4) 366 AA  
 TGF4\_HUMAN (Endometrial bleeding-associated factor) (Left-right determination factor A) (Lefty-A protein) [EBAF] [Homo sapiens (Human)] align

Score = 684 bits (1765), Expect = 0.0  
 Identities = 337/366 (92%), Positives = 337/366 (92%)

Query: 1 MWPLWLCWALWVLPLAGPGAALTXXXXXXXXXXXXVPLDRADMEKLVI PAHVRAQ 60  
 MWPLWLCWALWVLPLAGPGAALT VPVLDRADMEKLVI PAHVRAQ

Sbjct: 1 MWPLWLCWALWVLPLAGPGAALTEEQLLGSLLRQLQLSEVPVLDRADMEKLVI PAHVRAQ 60

Query: 61 YVVLRRSHGDRSRGKRFQSOSREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120  
 YVVLRRSHGDRSRGKRFQSOSREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL

Sbjct: 61 YVVLRRSHGDRSRGKRFQSOSREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120

Query: 121 FQEPPVKAALHRHGRILSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSHESGWKAFDV 180  
 FQEPPVKAALHRHGRILSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSHESGWKAFDV

Sbjct: 121 FQEPPVKAALHRHGRILSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSHESGWKAFDV 180

Query: 181 TEAVNFWXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQGAPAGLGE P QLELHTL 240  
 TEAVNFW VSVQREHLGPLASGAHKLVRFASQGAPAGLGE P QLELHTL

Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGE P QLELHTL 240

Query: 241 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQP 300  
 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQP

Sbjct: 241 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQP 300

Query: 301 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALV 360  
 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALV

Sbjct: 301 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALV 360

Query: 361 PRRLQP 366  
 PRRLQP

Sbjct: 361 PRRLQP 366

sp O75610 Left-right determination factor B precursor (Lefty-B) 366 AA  
 LFTB\_HUMAN protein (UNQ278/PRO317) [LEFTB] [Homo sapiens (Human)] align

Score = 654 bits (1688), Expect = 0.0  
 Identities = 323/366 (88%), Positives = 328/366 (89%)

Query: 1 MWPLWLCWALWVLPLAGPGAALTXXXXXXXXXXXXVPLDRADMEKLVI PAHVRAQ 60  
 M PLWLCWALWVLPLA PGAALT VP LDRADME+LVIP HVRAQ

Sbjct: 1 MQPLWLCWALWVLPLASPGAALTGEQLLGSLRLQLKEVPTLDRADMEELVIPHVRAQ 60

Query: 61 YVVLRRSHGDRSRGKRFQSOSREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120  
 YV LL+RSHGDRSRGKRFQSOSREVAGRFLA EASTHLLVFGMEQRLPPNSELVQAVLRL

Sbjct: 61 YVALLQRSHGDRSRGKRFQSOSREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRL 120

Query: 121 FQEPPVKAALHRHGRILSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSHESGWKAFDV 180

FQE PVPKAALHRHGRSLSPRSA+ARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV  
 Sbjct: 121 FQE PVPKAALHRHGRSLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180

Query: 181 TEAVNFXXXXXXVSVQREHLGPLASGAHKLVRFA\$QGAPAGLGE\$PQLELHTL 240  
 TEAVNFW VSVQREHLGPLASGAHKLVRFA\$QGAPAGLGE\$PQLELHTL  
 Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSQREHLGPLASGAHKLVRFA\$QGAPAGLGE\$PQLELHTL 240

Query: 241 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300  
 DL DYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTC+QP  
 Sbjct: 241 DLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCRQP 300

Query: 301 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALV 360  
 PEALAF WPFLGPRQCIASET SLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALV  
 Sbjct: 301 PEALAFKWPFLGPRQCIASETDSLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALV 360

Query: 361 PRRLQP 366  
 PRRLQP  
 Sbjct: 361 PRRLQP 366

tr Q8BMF7 Mus musculus 13 days embryo male testis cDNA, RIKEN full-length 368  
 enriched library, clone:6030463A22 product:LEFT-RIGHT AA  
 DETERMINATION FACTOR B (LEFTY-2 PROTEIN), full insert align  
 sequence (Endometrial bleeding associated factor) [Ebaif]  
 [Mus musculus (Mouse)]

Score = 567 bits (1461), Expect = e-160  
 Identities = 274/364 (75%), Positives = 299/364 (81%), Gaps = 2/364 (0%)

Query: 1 MWPLWLWVLPAGPGAA\$LTXXXXXXXXXXXXVPLDRADMEKLVI\$PAHVRAQ 60  
 M LWLWVLPAGPGAA+\$T P LD AD+E++ IP HVR+Q  
 Sbjct: 1 MKSLWLWVLPAGPGAA\$TEEQVLSSLLQQQLQLSQAPTLD\$ADVEEMAIPTHVRSQ 60

Query: 61 YV\$LLRRSHGDRSRGKRF\$QS\$REVAGRFLASEASTHLLVFGMEQR\$LP\$N\$ELVQAVLRL 120  
 YV LL+ SH DR\$RGKRF\$Q+\$REVAGRFL SE STHLLVFGMEQR\$LP\$N\$ELVQAVLRL  
 Sbjct: 61 YV\$LLRRSHGDRSRGKRF\$Q\$REVAGRFLMSETSTHLLVFGMEQR\$LP\$N\$ELVQAVLRL 120

Query: 121 FQE PVPKAALHRHGRSLSPRSQA\$ARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180  
 FQE PVP+ AL R RLSP SA+ARVT+EWLRVR+DGSNRT+LIDSRLVS+HESGWKAFDV  
 Sbjct: 121 FQE PVPRTALRRFERLSPHSARARVTIEWLRVREDGSNRTALIDSRLVSIHESGWKAFDV 180

Query: 181 TEAVNFXXXXXXVSVQREHLGPLASGAHKLVRFA\$QGAP--AGLGE\$PQLELH 238  
 TEAVNFW VSVQREHLGP AHKLVRFA+QG P G GE\$PQLELH  
 Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSQREHLGPGTWSAHKLVRFAAQGTPDGKGQGE\$PQLELH 240

Query: 239 TLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQ 298  
 TLDL+DYGAQG+CDPE P+TEGTRCCRQEMY+DLQGMKWAKNW+LEPPGFL YECVG+C  
 Sbjct: 241 TLDLKDYGAQGNCDPEPVTEGTRCCRQEMYLDLQGMKWAKNWILEPPGFLTYECVGSC 300

Query: 299 QPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGA 358  
 Q PE+L WPFLGPRQCIASETASLPMIVSIKEGGTRPQVVSLPNMRVQ KCSCASDGA  
 Sbjct: 301 QLPESLTIGWPFLGPRQCVASEMTSLPMIVSVKEGGTRPQVVSLPNMRVQTCSCASDGA 360

Query: 359 LVPR 362  
 L+PR

Sbjct: 361 LIPR 364

sp P57785 Left-right determination factor B precursor (Lefty-2) 368  
LFTB\_MOUSE protein AA  
[Leftb] [Mus musculus (Mouse)] align

Score = 565 bits (1455), Expect = e-160  
 Identities = 273/364 (75%), Positives = 298/364 (81%), Gaps = 2/364 (0%)

Query: 1 MWPLWLCWALWVLPLAGPGAA~~TXXXXXXXXXXXXX~~VPVLDRADMEKLVI~~PAHVRAQ~~ 60  
 M LWLCWALWVLPLAGPGAA+T P LD AD+E++ IP HVR+Q  
 Sbjct: 1 MKSLWLCWALWVLPLAGPGAA~~MTEEQVLSSLLQQQLQLSQAPT~~LDSADVEEMAI~~PTHVRSQ~~ 60

Query: 61 YV~~VLLRRSHGDRSRGKRF~~SQS~~FREVAGRFLASEASTHLLVFGMEQLPPNSELVQAVLRL~~ 120  
 YV LL+ SH DRSRGKRF~~SQ+~~ REVAGRFL SE STHLLVFGMEQLPPNSELVQAVLRL  
 Sbjct: 61 YV~~ALLQGSHADRSRGKRF~~SQNL~~REVAGRFLMSETSTHLLVFGMEQLPPNSELVQAVLRL~~ 120

Query: 121 FQEPVPKAALHRHGRLSPRSAQARVT~~VEWLVRDDGSNR~~TS~~LIDSRLVS~~HESGWKAFDV 180  
 FQEPVP+ AL R RLSP SA+ARVT+EWLRVR+DGSNRT+LIDSRLVS+HESGWKAFDV  
 Sbjct: 121 FQEPVPRTALRRFERLSPHSARARVT~~IEWLRVREDGSNRT~~ALIDSRLVS~~I~~HESGWKAFDV 180

Query: 181 TEAVNF~~WXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQGAP~~--AGLGE~~PQLELH~~ 238  
 TEAVNFW VSVQREHLGP AHKLVRFA+QG P G GEPQLELH  
 Sbjct: 181 TEAVNF~~WQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQGTPDGKGQGE~~PQLELH 240

Query: 239 TL~~DLRDYGAQGD~~C~~DPEAPMTEGTRCCRQEMYIDLQGMKWA~~N~~NWLEPPGFLAYECVGTCQ~~ 298  
 T~~LDL+DYGAQG+CDPE~~ P+TEGTRCCRQEMY+DLQGMKWA+NW+LEPPGFL YECVG+C  
 Sbjct: 241 TL~~DLKDYGAQGNCDPEVPVTEGTRCCRQEMYL~~D~~LQGMKWAENWILEPPGFLTYECVGSC~~L 300

Query: 299 QPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGG~~RTRPQVVS~~LPNM~~RVQKCSCASDGA~~ 358  
 Q PE+L WPFLGPRQC+ASE SLPMIVS+KEGG~~RTRPQVVS~~LPNM~~RVQ CSCASDGA~~  
 Sbjct: 301 QLPESLTIGWPFLGPRQCVA~~SEM~~TS~~LPMIVSVKEGG~~RTRPQVVS~~LPNM~~RVQTCSCASDGA 360

Query: 359 LVPR 362  
 L+PR  
 Sbjct: 361 LIPR 364

sp Q64280 Transforming growth factor beta 4 precursor (TGF-beta 4) 368  
TGF4\_MOUSE (Lefty AA  
 protein) (Lefty-1 protein) (STR A3 protein) (Ebaf) [Mus align  
 musculus (Mouse)]

Score = 556 bits (1432), Expect = e-157  
 Identities = 271/365 (74%), Positives = 295/365 (80%), Gaps = 2/365 (0%)

Query: 4 LWLCWALWVLPLAGPGAA~~TXXXXXXXXXXXXX~~VPVLDRADMEKLVI~~PAHVRAQYVV~~ 63  
 LWLCWALW L L ALT PVLD+AD+E +VIP+HVR QYV  
 Sbjct: 4 LWLCWALW~~ALSLVSLREALTGEQILGSLLQQQLQDQP~~VLDKADVEGMVIPSHVRTQYVA 63

Query: 64 LLRRSHGDRSRGKRF~~SQS~~FREVAGRFLASEASTHLLVFGMEQLPPNSELVQAVLRLFQE 123  
 LL+ SH RSRGKRF~~SQ+~~ REVAGRFL SE STHLLVFGMEQLPPNSELVQAVLRLFQE  
 Sbjct: 64 LLQHSHASRSRGKRF~~SQNL~~REVAGRFLV~~SETSTHLLVFGMEQLPPNSELVQAVLRLFQE~~ 123

Query: 124 PVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEA 183  
 PVP+ AL R RLSP SA+ARVT+EWLR RDDGSNRT+LIDSRLVS+HESGWKAFDVTEA  
 Sbjct: 124 PVPRTALRRQKRLSPHSARARVTIEWLRFRDDGSNRTALIDSRLVSIHESGWKAFDVTEA 183

Query: 184 VNFWXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAP--AGLGE PQLELHTLD 241  
 VNFW VSVQREHLGP +HKLVRFA+QG P G GEPQLELHTLD  
 Sbjct: 184 VNFWQQLSRPRQPLLLQVSVQREHLGPGTWSSHKLVRFAAQGT PDGKGQGE PQLELHTLD 243

Query: 242 LRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPP 301  
 L+DYGAQG+CDPEAP+TEGTRCCRQEMY+DLQGMKWA+NW+LEPPGFL YECVG+C Q P  
 Sbjct: 244 LKDYGAGQGNCDPEAPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSCQLP 303

Query: 302 EALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVP 361  
 E+L WPFLGPRQC+ASE SLPMIVS+KEGGRTRPQVVSLPNMRVQ CSCASDGAL+P  
 Sbjct: 304 ESLTSRWPFLGPRQCVASEMSTSLPMIVSVKEGGRTRPQVVSLPNMRVQTCSCASDGALIP 363

Query: 362 RRLQP 366  
 RRLQP  
 Sbjct: 364 RRLQP 368

tr Q9DFC6 TGF-beta family member lefty-A [Xenopus laevis (African clawed frog)]

align

Score = 232 bits (592), Expect = 7e-60  
 Identities = 126/330 (38%), Positives = 193/330 (58%), Gaps = 16/330 (4%)

Query: 40 VPVLDRADMEKLVPAHVRAQYVVLRRSHGDRSRGK-----RFSQSREVAGRFLA 91  
 VP L++ D+E LVIP H++A+Y+ +L SH +R R R +++G L  
 Sbjct: 43 VPKLEKRDVENLVI PRHIQAKYMSMLH-SHRERKRRSLPSLAGILRGISGNADISGEILY 101

Query: 92 SEASTHLLVFGMEQRLLPPNSELVQAVLRLFQE PVPKAALHRHGRLSPRSAQARVTVEWLR 151  
 S++S +VFGME R+P NSE+ A L+LF++P PK R + ARV+V ++  
 Sbjct: 102 SDSSKQTMVFGMESRI PENSEVTMAELKLFKKP-PKIMNPERRFHRSVSNARVSVYYVE 160

Query: 152 VRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFXXXXXXVSVQREHLGPL 211  
 + DG+NRTSL+DSRLV + ESGW++FDVT+AV++W + V E G  
 Sbjct: 161 ILKDGTNRTSLVDSRLVPIMESGWRSFDVTQAVHYW-MKSGGHSSMHLEIHVDGERHGSH 219

Query: 212 ASGAHKLVRFASQG-APAGLGE PQUELHTLDRDYGAQGDCDPEAPMTEGTRCCRQEMYI 270  
 AS K+VRF +Q + LG+P+L L TL+L ++GA+GDC + CCR+E +I  
 Sbjct: 220 ASEMAKMVRFTTQS PSDNSL GKPELV LFTLN LDEHGARGDCSASGAKKDNI-CCREYFI 278

Query: 271 DLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQCIASETASLPMIVSI 330  
 + + + W + W++EP G+ A+ C G+C+QP L+ ++ G R C E+A LP++ +  
 Sbjct: 279 NFRELTWTQYWIIEPAGYNAFR CAGSCKQPKYPLSHHY---GERMC AVVESAPLPVMYLV 335

Query: 331 KEGGRTRPQVVSLPNMRVQKCSCASDGALV 360  
 K+G T +V PNM V+KC C D +  
 Sbjct: 336 KKGDYTEIEVAEFPNMIVEKCGCTMDNIAI 365

tr Q9DD36 Xantivin (Lefty-related factor Xatv) [Xantivin] [Xenopus laevis] 367 AA

**(African clawed frog)**

align

Score = 229 bits (583), Expect = 8e-59  
 Identities = 128/337 (37%), Positives = 190/337 (55%), Gaps = 29/337 (8%)

Query: 40 VPVLDRADMEKLVI PAHVRAQYVVLLRRSHGDRSRGKRFQSFR-----EVAGRF 89  
 VP L++ D+E LVIP H++A+Y+ +L H R R KR S +++G  
 Sbjct: 43 VPKLEKRDVENLVI PGHIQAKYMSML--HNHRERKKRSLPSLAGILRGISGNADISGEI 99

Query: 90 LASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP----VPKAALHRHGRILSPRSAQAR 144  
 L S++S LVFGME R+P NSE+ A L+LF++P VP+ HR AR  
 Sbjct: 100 LYSDSSKQSLVFGMESRIPENSEVTMAELKLFKKPKIMNVPERRFHRPVN-----NAR 153

Query: 145 VTVEWLVRDDGSNRTSLIDSRVLVS VHESGWKA F D V T E A V N F W X X X X X X X X V S V Q 204  
 V+V ++ + DG+NRTSL+DSRLV + ESGW++FDVT+AV++W + V  
 Sbjct: 154 VSVYYVEILKDGTNRTSLVDSRLVPIMESGWRSFDVTQAVHYW-MRSGGQSSMHLEIHVD 212

Query: 205 REHLGPLASGAHKLVRFASQG-APAGLGE P Q L E L H T L D L R D Y G A Q G D C D P E A P M T E G T R C 263  
 E G AS K+VRF +Q + LG+P+L L TL+L + G +GDC + C  
 Sbjct: 213 GERHGSHASEMAKMVRFTTQS P SDNSLGKPELVLFTLN LNEQGTRGDCSASGAKKDNI-C 271

Query: 264 CRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT C Q P P E A L A F N W P F L G P R Q C I A S E T A S 323  
 CR+E +I+ + + W + W++EP G+ A+ C G+C+QP L+ G R C E+A  
 Sbjct: 272 CREEYFINFRELWTQYWIIEPAGYNAFRCTGSCKQPKYPLSHY--HYGQRTCAVVESAP 329

Query: 324 LPMIVSIKEGGTRPQVVS LPNMRVQKCSCASDGALV 360  
 LP++ +K+G T +V PNM V+KC C D +  
 Sbjct: 330 LPVMYLVKKGDYTEIEVAEFPNMIVEKGCGCTMDNIAI 366

tr Q9DFC5 TGF-beta family member lefty-B [Xenopus laevis (African clawed frog)]

align

Score = 228 bits (582), Expect = 1e-58  
 Identities = 128/337 (37%), Positives = 190/337 (55%), Gaps = 29/337 (8%)

Query: 40 VPVLDRADMEKLVI PAHVRAQYVVLLRRSHGDRSRGKRFQSFR-----EVAGRF 89  
 VP L++ D+E LVIP H++A+Y+ +L H R R KR S +++G  
 Sbjct: 43 VPKLEKRDVENLVI PRHIQAKYMSML--HNHRERKKRSLPSLAGILRGISGNADISGEI 99

Query: 90 LASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP----VPKAALHRHGRILSPRSAQAR 144  
 L S++S LVFGME R+P NSE+ A L+LF++P VP+ HR AR  
 Sbjct: 100 LYSDSSKQSLVFGMESRIPENSEVTMAELKLFKKPKIMNVPERRFHRPVN-----NAR 153

Query: 145 VTVEWLVRDDGSNRTSLIDSRVLVS VHESGWKA F D V T E A V N F W X X X X X X X X V S V Q 204  
 V+V ++ + DG+NRTSL+DSRLV + ESGW++FDVT+AV++W + V  
 Sbjct: 154 VSVYYVEILKDGTNRTSLVDSRLVPIMESGWRSFDVTQAVHYW-MRSGGQSSMHLEIHVD 212

Query: 205 REHLGPLASGAHKLVRFASQG-APAGLGE P Q L E L H T L D L R D Y G A Q G D C D P E A P M T E G T R C 263  
 E G AS K+VRF +Q + LG+P+L L TL+L + G +GDC + C  
 Sbjct: 213 GERHGSHASEMAKMVRFTTQS P SDNSLGKPELVLFTLN LNEQGTRGDCSASGAKKDNI-C 271

Query: 264 CRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT C Q P P E A L A F N W P F L G P R Q C I A S E T A S 323  
 CR+E +I+ + + W + W++EP G+ A+ C G+C+QP L+ G R C E+A  
 Sbjct: 272 CREEYFINFRELWTQYWIIEPAGYNAFRCTGSCKQPKYPLSHY--HYGQRTCAVVESAP 329

Query: 324 LPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV 360  
 LP++ +K+G T +V PNM V+KC C D +  
 Sbjct: 330 LPVMYLVKKGDYTEIEVAEFPNMIVEKCGCTMDNIAI 366

**tr Q9PVN4**      **Lefty [Gallus gallus (Chicken)]**      **362 AA align**

Score = 226 bits (575), Expect = 7e-58  
 Identities = 131/352 (37%), Positives = 187/352 (52%), Gaps = 8/352 (2%)

Query: 10 LWVLPLAGPGAALTXXXXXXXXXXXXVPLDRADMEKLVI PAHVRAQYVVLLRRSH 69  
 L+VL L A T VP L + D+ LVIP HV+ +Y+ +L+R  
 Sbjct: 9 LYVLCLVAMACAFQEGFKEVMLKQLGLSEVPKLHKRDLVDLVIPEHVKNKYISMLKRHR 68

Query: 70 GDRSRGKRESQSFRREVAGR--FLASEASTHLLVFGMEQRLLPPNSELVQAVLRLFQEPPVK 127  
 G R + + G S+ +F ME R+P NSE+ A L+LF++P+ +  
 Sbjct: 69 GKRRASPSLASILQGIPGNAEVFYSDPMRQNFI FDMEGRIPKNSEVTMAELKLFKKPLDR 128

Query: 128 AALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSHESGWKAFCDVTEAVNFW 187  
 L P S ARV++ W++ + DG+NRTSLIDSRLV + ESGWK FDVT+AV++W  
 Sbjct: 129 VNLPARQPHRPVS-NARVSIYVWQRQHDGTNRTSLIDSRLVPIRESGWKNFDVTQAVHYW 187

Query: 188 XXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFAAQGA-PAGLGEQLELHTLDLRDYG 246  
 V ++ E + A+ K VRF SQ A +G P+L L+TLDL DYG  
 Sbjct: 188 -LRNKROEPMVLOQWIEGERVASYAAEVAKSVRFTSQDAGDRAVGRPELVLYTLDLEDYG 246

Query: 247 AQGDCDPPEAPMTEGTRCCRQEMYIDLQGMKWAKNWLEPPGFLAYECVGTCCQQPPEALAF 306  
 GDC + T CCRQ+ YI+ + + W + WV+EP G+ AY C G C Q P L  
 Sbjct: 247 GPGDCKDGVQAGKST-CCRQKHYINFRELSWTQYWVIEPAGYQAYSCRGGLQPLGPLQL 305

Query: 307 NWPFGLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGA 358  
 W R C +E++ LP++ ++ G T + PNM ++KCSC +DGA  
 Sbjct: 306 -WGG-RERACAVAESSPLPIMYLVRGNHTEIEATEFPNMIIEKCSMADGA 355

**tr Q9W6I7**      **Signaling molecule lefty2 [lft2] [Brachydanio rerio (Zebrafish) (Danio rerio)]**      **362 AA align**

Score = 219 bits (559), Expect = 5e-56  
 Identities = 121/330 (36%), Positives = 183/330 (54%), Gaps = 25/330 (7%)

Query: 41 PVLDRADMEKLVI PAHVRAQYVVLLRRSHGDRSRGK-----RFSQSFRREVAGRFLASE 93  
 P + + D+E LV+PAH+++Y+ +L+ H R R R + + G S+  
 Sbjct: 39 PRIQKRDLENLVVPAHIKS KYLSMLKLHHQRRRSLPSLAGILRGHGNADITGEIKYSD 98

Query: 94 ASTHLLVFGMEQRLLPPNSELVQAVLRLFQEPPV--PKAALHRHGRLSPRSAQARVTVEWLR 151  
 + LVF ME RL N+E+ A L+LFQ P RH R ARV++ W+  
 Sbjct: 99 TTRQRLVFDMEARLQENTEVTM AELKLFQTAQSPSKPERRHHR---PINHARVSIYWVE 155

Query: 152 VRDDGSNRTSLIDSRLVSHESGWKAFCDVTEAVNFXXXXXXXXXVSVQREHLGPL 211  
 V ++GSNRTSL+DSRLV +HESGW++FDVT+A+++W V + E G  
 Sbjct: 156 VLENGSNRTSLLDSRLVPIHESGWRSFDVTQAIHYW-SKSQKKAPLHLEVWTEGERPGSY 214

Query: 212 ASGAHKLVRFASQGAPAG-----LGEHQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQ 266  
 A+ K VRFA+Q +G P+L L+TLDL +YG+QG+C+ ++CCR+  
 Sbjct: 215 AAEMAKRVRATQDPKENTLEKDMGAPELVLYTLDLDEYGSQGNCCNS---PNSSKCCRE 271

Query: 267 EMYIDLQGMKWAKNWVLEPPGFLAYECVGTCCQQPPEALAFNWPFLGPRQCIASETASLPM 326  
 E +I+ + + W +W++EP G+ A+ C G C+QP + G R C E+A LPM  
 Sbjct: 272 EHFINFRELWTQYWIIEPAGYQAFCRCAAGGCKQPKR----GFYGYGQRTCAVMESAPLPM 327

Query: 327 IVSIKEGGRTRPQVVSLPNMRVQKCSCASD 356  
 + +K+G T +V PNM V+KC C+ D  
 Sbjct: 328 MYLVKKGDYTEIEVAEFPNMIVEKGCSMD 357

tr Q9PW55 Antivin [lft1] [Brachydanio rerio (Zebrafish) (Danio rerio)] 358 AA

align

Score = 219 bits (559), Expect = 5e-56  
 Identities = 115/329 (34%), Positives = 185/329 (55%), Gaps = 18/329 (5%)

Query: 40 VPVLDRADMEKLVI PAHVRAQYVVLLRRSHGDRSRGK-----RFSQSREVAGRFLAS 92  
 +P + + D+E LVIP HV+ +Y+ +L+ H + R R +++G F+ S  
 Sbjct: 39 IPQIHKRDLENLVI PTHVKNKYISMLKLHHSRKRRSLPSLAGILRGIPGNADISGEFVYS 98

Query: 93 EASTHLLVFGMEQRLLPPNSELVQAVLRLFQE PVPKAALHRHGRLSPRSAQARVTVEWLRV 152  
 + + +VF M R+P NSE+ A L+L+++ K ++ P + ARV++ W+  
 Sbjct: 99 DTTRQRVVFEMTSRIPENSEVTMAELKLYKKAPHKRSI PERKGHRPVN-NARVSIYWVEP 157

Query: 153 RDDGSNRTSLIDSRLVSVHESGWKA FDVTEAVNFWXXXXXXXXXXXXXSVQREHLGPLA 212  
 + DGSNRTSL+DSRL+ +HE+GWK+FDVT+AV +W V ++ E G A  
 Sbjct: 158 QKDGSNRTSLVDSRLIPIHETGWKSFDVTQAVQYW-SRSRMEMPMHLEVWIEGERPGSYA 216

Query: 213 SGAHKLVRFASQGAPAG-LGEHQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYID 271  
 + K V F +Q LG+P+L L+TLDL ++G+ GDC+ + CCR++ +I+  
 Sbjct: 217 AEMAKCVHFTTQDPDDNTLGKPELVLYTLNLEFGSSGDCENN--KDREMCCREQYFIN 273

Query: 272 LQGMKWAKNWVLEPPGFLAYECVGTCCQQPPEALAFNWPFLGPRQCIASETASLPMIVSIK 331  
 + + W +W++EP G+ A+ C G C+QP + G R+C E+A LPM+ +K  
 Sbjct: 274 FRALTWTQYWIIEPSGYQAFCRCKGGCRQPKRNYGY----GERKCAVVESAPLPMMLVK 328

Query: 332 EGGRTRPQVVSLPNMRVQKCSCASDGALV 360  
 +G T +V PNM V+KC CA D V  
 Sbjct: 329 KGDYTEIEVAEFPNMIVEKGCGCAMDNISV 357

tr Q9PUK3 LEFTY-1 protein (Fragment) [LEFTY-1] [Gallus gallus (Chicken)] 320 AA

align

Score = 218 bits (556), Expect = 1e-55  
 Identities = 122/317 (38%), Positives = 177/317 (55%), Gaps = 8/317 (2%)

Query: 45 RADMEKLVI PAHVRAQYVVLLRRSHGDRSRGKRF SQSFREVAGR--FLASEASTHLLVFG 102  
 + D+ LVIP HV+ +Y+ +L+R G R + + + G S+ +F  
 Sbjct: 2 KRDLVDLVIPEHVKNKYISMLKRH RGKRRASP SLASILOQGIPGNAEVFYSDPMRQNIFD 61

Query: 103 MEQRLPPNSELVQAVLRLFQE PVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSL 162  
 ME R+P NSE+ A L+LF++P+ + L P S ARV++ W++ + DG+NRTSL  
 Sbjct: 62 MEGRIPKNSEVMTMAELKLFKKPLDRVNLPARQPHRPVS-NARVSIYWWVQRQHDGTNRTSL 120

Query: 163 IDSRLVSVHESGWKAFDVTEAVNFXXXXXXVSVQREHLGPLASGAHKLVRFA 222  
 IDSRLV + ESGWK FDVT+AV++W V ++ E + A+ K VRF  
 Sbjct: 121 IDSRLVPIRESGWKNFDTQAVHYW-LRNKRQEPMVLQVWIEGERVASYAAEVAKSVRFT 179

Query: 223 SQGA-PAGLGEPOLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNW 281  
 SQ A +G P+L L+TLDL DYG GDC + T CCRQ+ YI+ + + W + W  
 Sbjct: 180 SQDAGDRAVGRPELVLYTLDEDYGGPGDCKDGVQAGKST-CCRQKHYINFRELSWTQYW 238

Query: 282 VLEPPGFLAYECVGTCCQQPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVV 341  
 V+EP G+ AY C G C Q P L W R C +E++ LP++ ++ G T +  
 Sbjct: 239 VIEPAGYQAYSCRGGLQLPGPLQL-WGG-RERACAVAESSPLPIMYLVRGNHTEIAT 296

Query: 342 SLPNMRVQKCSCASDGA 358  
 PNM ++KCSC +DGA  
 Sbjct: 297 EFPNMIIEKCSCMADGA 313

tr Q9W6I6 Signaling molecule lefty1 [lft1] [Brachydanio rerio] 358  
 (Zebrafish)  
 (Danio rerio) AA align

Score = 217 bits (552), Expect = 3e-55  
 Identities = 114/329 (34%), Positives = 185/329 (55%), Gaps = 18/329 (5%)

Query: 40 VPVLDRADMEKLVI PAHVRAQYVVLRRSHGDRSRGK-----RFSQSREVAGRFLAS 92  
 +P + + D+E LVIP +V+ +Y+ +L+ H + R R +++G F+ S  
 Sbjct: 39 IPQIHKRDLLENLVIPTNVKNKYISMLKLHHSRKRRSLPSLAGILRGIPGNADISGEFVYS 98

Query: 93 EASTHLLVFGMEQRLPPNSELVQAVLRLFQE PVPKAALHRHGRLSPRSAQARVTVEWLRV 152  
 + + +VF M R+P NSE+ A L+L++ K ++ P + ARV++ W+  
 Sbjct: 99 DTTRQRVVFEMTSRIPENSEVTMAELKLYKKAPHKRSI PERKGHRPVN-NARVSIYWEP 157

Query: 153 RDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFXXXXXXVSVQREHLGPLA 212  
 + DGSNRTSL+DSRL+ +HE+GWK+FDVT+AV +W V ++ E G A  
 Sbjct: 158 QKDGSNRTSLVDSRLIPIHETGWKSFDVTQAVQYW-SRSRMEMPMHLEVWIEGERPGSYA 216

Query: 213 SGAHKLVRFA\$QGAPAG-LGE\$PQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYID 271  
 + K V F +Q LG+P+L L+TL+L ++G+ GDC+ + CCR++ +I+  
 Sbjct: 217 AEMAKCVHFTTQDPDDNTLGKPELVLYTLNLEFGSSGDCENN--KDREMCCREQYFIN 273

Query: 272 LQGMKWAKNWVLEPPGFLAYECVGTCCQQPPEALAFNWPFLGPRQCIASETASLPMIVSIK 331  
 + + W + W++EP G+ A+ C G C+QP + G R+C E+A LPM+ +K  
 Sbjct: 274 FRALTWTQYWIIEPSGYQAFRCKGGCRQPKRNYGY----GERKCAVVESAPLPMMYLVK 328

Query: 332 EGGRTRPQVVS LPNMRVQKCSCASDGALV 360  
 +G T +V PNM V+KC CA D V  
 Sbjct: 329 KGODYTEIEVAEFPNMIVEKCGCAMDNISV 357

tr Q95YK6 Lefty/antivin related protein [Cs-lfan] [Ciona 372 AA

savignyi] align

Score = 145 bits (366), Expect = 1e-33  
 Identities = 107/348 (30%), Positives = 160/348 (45%), Gaps = 43/348 (12%)

Query: 40 VPVLDRADMEKLVI PAHVRAQYVVLLRR-SHGDRSRGKRFQS-FREV-----AGRFLA 91  
       VP      ++ +VIP   R +Y   ++ + + +R+R    Q   FR V            G +  
 Sbjct: 32 VPRFTHNEVRNVVIPDETRRKYERMKTLERNRRSSSLQDLFRSVHKKTGIEGDVIY 91

Query: 92 SEASTHLLVFGMEOQLPPNSELVQAVLRLFQE PVPKAALHRHGRL----- 136  
       S+      L F ME RLP + + A LRLF++            L H R+  
 Sbjct: 92 SDTFREELKFDMEGRLPDDYMISMAELRLFKK-----LPNHNRLSRLTPSGNRNDVQ 145

Query: 137 --SPRSAQ----ARVTVEWLRVRDDGSNRTSLIDSRLVS VHESGWKA F DVTEAVNFWXX 189  
       S R    Q    ARV++           DG   T L+DSRL+ V+ SGW   FDVT A+ W  
 Sbjct: 146 LSSARGRQQVIRNARVSIHLSLPLPDGGAVTELVDTRLILVNGSGWHTFDVTSAIRKWRR 205

Query: 190 XXXXXXXXXXXXVS VQREHLGPLASGAHKLVRFASQG-APAGLGE P QLE LHTLDLRDYGAQ 248  
       + VQ    G A+    +L+RF Q A            P+L ++T + ++  
 Sbjct: 206 HPVRYMTITLELK VQSSSPGRAAAE LARLIRFTGQRVALDSPRRPELVVYT-NAKEPART 264

Query: 249 GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQPPEALAFNW 308  
       DC      + +CCR+    +++ + KW+K+W+LEP GF AY C G C+ , +  
 Sbjct: 265 SDCSSSRHNRQH-KCCRENRFVNFR ETKWSKH WILEPAGFNAYHCAGGC RSDRRNSKG- 322

Query: 309 PFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASD 356  
       PR C A+ET SLP++ +K+GG    +V    PNM ++KCSA D  
 Sbjct: 323 ---APRSCSATETNSLPI MLYVKKGAIHVEVSEFPNMVIEKCSCALD 367

tr Q6T265 **Antivin/lefty [Paracentrotus lividus (Common sea urchin)]** 404 AA

align

Score = 103 bits (256), Expect = 6e-21  
 Identities = 89/359 (24%), Positives = 138/359 (37%), Gaps = 60/359 (16%)

Query: 47 DMEKLVI PAHVRAQYVVLLRRSHGDRSRGKRFQS FREVAGRFLASEASTHLLVFGMEOQR 106  
       D    L +P H+R QY   + R+    R+    +    E+ G    +E +    L F +  
 Sbjct: 52 DASTLTVPDHLRFQYESMHRQHRVRRAYITKG IHNKEE IYGEVSYTERNRQLFTFDI SS- 110

Query: 107 LPPNSELVQAVLRLFQE-----PVPKAALHRHGRLSPRSAQARVT----- 146  
       +P    SE++ A L++++E                           P +    H H    + S + V  
 Sbjct: 111 IPEGSEVIMAELKVYKERPNHSIFKPEGE EGEAPHSNNHDHVHSALVSIKQLVDQEV DMD 170

Query: 147 VEWLVRDDGSNR-----TSLIDSRLVS VHESGWKA F DVTEAVNFWXXXXXXXXXXV 201  
       E    + D+ N+    T ID R +++ +GWK FDVT + W  
 Sbjct: 171 AE PADLADEVVNQHDGMDTITIDQREM TLKGAGWKVFDVTNTI QTWVADSDSNLGVAL-- 228

Query: 202 SVQREHLGPLASGAHKL----VRFASQGAPAGLGE P QLE LHTLDLRDYGAQGDCDPEAP 256  
       H+ P+ G H    + FA+    P    P    +    A    +P  
 Sbjct: 229 -----HIDPIEGGHHAQQVVDEMVFATDFFPETPDSRPV LVIYTTKYAPASDEPNEC 283

Query: 257 MTEGT---RCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQPPEAL---AFNWP F 310  
       EG    RCCR+ Y+D + + W    W++EP GF A++C G C P            F PF  
 Sbjct: 284 RYE GEEEHRCRRK YVDFRDLSWTSR WIIEPAGFEAFDCYGPCHNPRSRHIRDVFR LPF 343

Query: 311 LGP-----RQCIASETASLPMI-VSIKEGGRTRPQVSLPNMRVQKCSC 353  
          G    
                          R C S ++SLPM+ +S   G       +V    +PNM V+ C C  
Sbjct: 344 FGASSSGSSIFGAGSGGHRTCGVSRSSSLPPMMYLSETPSGTVELKVEEIPNMIVEDCGC 402

tr Q767A1 Signalng molecule lefty1 (Fragment) [lefty1] [Oryzias latipes 112 AA  
(Medaka fish) (Japanese ricefish)] align

Score = 84.0 bits (206), Expect = 4e-15  
Identities = 41/115 (35%), Positives = 66/115 (56%), Gaps = 5/115 (4%)

Query: 170 VHESGWKA~~F~~DVT~~E~~AVNFXXXXXXVSVQREH~~L~~G~~P~~LA~~S~~GA~~H~~KLVRFASQGAPAG 229  
+HE+GWK+FDVT+AV++W V ++ E G A+ K VRF +Q  
Sbjct: 2 IHETGWKS~~F~~DVTQAVHYW-SKTOOKTPMHLEVWIEGERPGSYAAEVAKSVRFTTQEOTEH 60

Query: 230 L-GEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMWKAKNWVL 283  
          G+P+L L+TL+L +YG++GDCD CCR++ +ID + + W + W++  
Sbjct: 61 TSGKPELVLYTLNLEEYGSRGDCD---VYQSKDTCCREOYFIDFRALTWTQYWI 112

tr Q9XYQ7 Bone morphogenetic protein BMP2/4 [BMP2/4] [Lytechinus variegatus (Sea urchin)] 417 AA align

Score = 69.3 bits (168), Expect = 1e-10  
Identities = 70/280 (25%), Positives = 110/280 (39%), Gaps = 47/280 (16%)

Query: 60 QYVVILLRRSHGDRSRGKRFQS F-----REVAGRFLASEASTHLLVFGME 104  
 QY++ L RSH + G F E AG+ L +E H ++F +  
 Sbjct: 81 OYMMMDLYRSHTEHODGISMHFEDFHLSTGTANTIRSYHHEDAGOVLPTEEHHBRTVILENIS 140

Query: 105 QRLPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSA-----QARVTVEWLVR RDDGSN 158  
 +P L A L R L F + + + + + L R + R + V + + + N  
 Sbjct: 141 T-MPAEEFVLTMAELRLFEKDL EEFHSTAKRHALDDRKSLSI PTHYMO RINVEHT -LKPVARN 198

Query: 159 RTS---LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXVSVQREHLGPLASGA 215  
 R + LID+RLV V ' S W++FDV AV W + . R P  
 Sbjct: 199 PDTIKRILDTLVDPVNSWESFDVPAVTWSWVEPKNUCLEILELIDSRCGRPSR N 254

Query: 216 HKLVRFASQGAPAGLGEPQLELHTL-----DLRDYGAQGDCDPEAPMTEGTR----- 262  
H VR + P+ + E Q E + Y G +P + G +  
Sbjct: 255 IWWVIVTREDFPSKIVQELQNEEDERWEEFTDQLVTKSDGCP TKDSCGCGCGRGIVKSYK 312

Query: 263 --CCRQEMYIDLQGMWKAWNWLLEPPGFLAYECVGTCCQP 300  
C R +Y+D + W +W++ P G+ AY C G C P  
Sbjct: 214 ANGCRQEMYIDLQGMWKAWNWLLEPPGFAYECVGTCCQP 300

tr Q8JIJ4 Bmp4 protein [Bmp4] [Steatocranus casuarius (lionhead cichlid)] 403 AA align

Score = 67.4 bits (163), Expect = 4e-10  
 Identities = 60/205 (29%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQAR VTV-EWLRVRDDGSNRTSLIDS 165  
 +P + L A LRL++ + +A +S A R+ V E L+ G T L+DS  
 Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA--ISDDQALHRINVYEVLKAPRPGQLITQLLD 201

Query: 166 RL VSVHESGWKA F D VTEAVNF WXXXXXXXXXXXXV SVQREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +  
 Sbjct: 202 RL VRHN ASRWE SF DVSPAVL RW--TRERLPNYGLAVEVLHLNQT PRH QGRHVRISRS LHQ 259

Query: 226 APAGLGE PQLELHTLDL RDYGAQGD CDP-----EAPMTEGTR---CCRQEMYIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +  
 Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRS PRQR GRKR N RN CRR HALYVDFSDV 315

Query: 276 KWAKNWVLE PPGFLAYECVGTCQQP 300  
 W +W++ PPG+ AY C G C P  
 Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339

tr Q8JIK1 Bmp4 protein [Bmp4] [Ctenochromis horei] 403 AA  
align

Score = 66.6 bits (161), Expect = 7e-10  
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQAR VTV-EWLRVRDDGSNRTSLIDS 165  
 +P + L A LRL++ + +A +S A R+ V E L+ G T L+DS  
 Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA--ISDDQALHRINVYEVLKAPRPGQLITQLLD 201

Query: 166 RL VSVHESGWKA F D VTEAVNF WXXXXXXXXXXXXV SVQREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +  
 Sbjct: 202 RL VRHN ASRWE SF DVSPAVL RW--TRERLPNYGLAVEVLHLNQT PRH QGRHVRISRS LHQ 259

Query: 226 APAGLGE PQLELHTLDL RDYGAQGD CDP-----EAPMTEGTR---CCRQEMYIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +  
 Sbjct: 260 EP---GEDWKQLRPL-LVTFGHDGKGHPLTRRTKRS PRQR GRKR N RN CRR HALYVDFSDV 315

Query: 276 KWAKNWVLE PPGFLAYECVGTCQQP 300  
 W +W++ PPG+ AY C G C P  
 Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339

tr Q78DH6 Bmp4 protein [Bmp4] [Gnathochromis permaxillaris] 403 AA  
align

Score = 66.2 bits (160), Expect = 9e-10  
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQAR VTV-EWLRVRDDGSNRTSLIDS 165  
 +P + L A LRL++ + +A +S A R+ V E L+ G T L+DS  
 Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA--ISDDQALHRINVYEVLKAPRPGQLITQLLD 201

Query: 166 RL VSVHESGWKA F D VTEAVNF WXXXXXXXXXXXXV SVQREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +

Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +

Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTQQP 300

W +W++ PPG+ AY C G C P

Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q78DH5 **Bmp4 protein [Bmp4] [Haplotaodon microlepis]** 403 AA  
align

Score = 66.2 bits (160), Expect = 9e-10

Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165  
 +P + L A LRL++ + +A +S A R+ V E L+ G T L+D+

Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPQQLITQLDT 201

Query: 166 RLVSVHESGWKA FDVTEAVNFWXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +

Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +

Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTQQP 300

W +W++ PPG+ AY C G C P

Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q78DH4 **Bmp4 protein [Bmp4] [Ophthalmotilapia nasuta]** 403 AA  
align

Score = 66.2 bits (160), Expect = 9e-10

Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165  
 +P + L A LRL++ + +A +S A R+ V E L+ G T L+D+

Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPQQLITQLDT 201

Query: 166 RLVSVHESGWKA FDVTEAVNFWXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +

Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +

Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTQQP 300

W +W++ PPG+ AY C G C P

Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q78DH3 Bmp4 protein [Bmp4] [Tanganicodus irsacae (Spotfin goby cichlid)] 403  
AA  
align

Score = 66.2 bits (160), Expect = 9e-10  
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQAR VTV-EWLRVRDDGSNRTSLIDS 165  
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+  
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPQQLITQLLDT 201

Query: 166 RLVS VHESGWKA FDVTEAVNFWXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225  
RLV + S W++FDV+ AV W V V + P G H + +  
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRS LHQ 259

Query: 226 APAGLGE P QLELHTLDLRDYGAQGD CDP-----EAPMTEGTR----CCRQEMYIDLQGM 275  
P GE +L L L +G G P +P G + C R +Y+D +  
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRS PRQRGRKRN RNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGT CQQP 300  
W +W++ PPG+ AY C G C P  
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339

tr Q8JIK2 Bmp4 protein [Bmp4] [Astatoreochromis alluaudi (Alluaud's haplo)] 403  
AA  
align

Score = 66.2 bits (160), Expect = 9e-10  
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQAR VTV-EWLRVRDDGSNRTSLIDS 165  
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+  
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPQQLITQLLDT 201

Query: 166 RLVS VHESGWKA FDVTEAVNFWXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225  
RLV + S W++FDV+ AV W V V + P G H + +  
Sbjct: 202 RLVGHNNSRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRS LHQ 259

Query: 226 APAGLGE P QLELHTLDLRDYGAQGD CDP-----EAPMTEGTR----CCRQEMYIDLQGM 275  
P GE +L L L +G G P +P G + C R +Y+D +  
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRS PRQRGRKRN RNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGT CQQP 300  
W +W++ PPG+ AY C G C P  
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339

tr Q8JIJ9 Bmp4 protein [Bmp4] [Haplochromis burtoni (Burton's mouthbrooder)] 403  
AA  
align

Score = 66.2 bits (160), Expect = 9e-10  
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQAR VTV-EWLRVRDDGSNRTSLIDS 165  
 +P + L A LRL++ + +A +S A R+ V E L+ G T L+D+  
 Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RL VSVHESGWKA F D VTEAVNF WXXXXXXXXXXXXV S V QREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +  
 Sbjct: 202 RL VRHN ASRWE SF D VSPAVL RW--TRERLPNYGLAVEVLH L NQT PRH QGRH VRIS RSLHQ 259

Query: 226 APAGLGE P QLE LHT L D L R DY GA QGD CDP-----EAPMTEGTR----CCRQEM YIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +  
 Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHP LTR RTKRS PRQR GRKR NRNC RRHALYVDFSDV 315

Query: 276 KWAKNWVLE P P GFLAYECVGTCQQP 300  
 W +W++ PPG+ AY C G C P  
 Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339

tr Q8JIJ6 Bmp4 protein [Bmp4] [Labidochromis caeruleus (blue streak  
 hap)] 403  
 AA  
align

Score = 66.2 bits (160), Expect = 9e-10  
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQAR VTV-EWLRVRDDGSNRTSLIDS 165  
 +P + L A LRL++ + +A +S A R+ V E L+ G T L+D+  
 Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RL VSVHESGWKA F D VTEAVNF WXXXXXXXXXXXXV S V QREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +  
 Sbjct: 202 RL VRHN ASRWE SF D VSPAVL RW--ARERLPNYGLAVEVLH L NQT PRH QGRH VRIS RSLHQ 259

Query: 226 APAGLGE P QLE LHT L D L R DY GA QGD CDP-----EAPMTEGTR----CCRQEM YIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +  
 Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHP LTR RTKRS PRQR GRKR NRNC RRHALYVDFSDV 315

Query: 276 KWAKNWVLE P P GFLAYECVGTCQQP 300  
 W +W++ PPG+ AY C G C P  
 Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339

tr Q8JIJ2 Bmp4 protein [Bmp4] [Tilapia rendalli (redbreast tilapia)] 403 AA  
align

Score = 66.2 bits (160), Expect = 9e-10  
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQAR VTV-EWLRVRDDGSNRTSLIDS 165  
 +P + L A LRL++ + +A +S A R+ V E L+ G T L+D+  
 Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKA~~F~~DVTEAVNFXXXXXXV~~S~~VQREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +  
 Sbjct: 202 RLVRHN~~A~~RWESFDVSPAVLRW--THERLPNYGLAVEVLH~~L~~NQT~~P~~RHQGRHVRISRSLHQ 259

Query: 226 APAGLGE~~P~~QLELHTLDLRDYGAQGDCDP-----EAPMTEGTR---CCRQEMYIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +  
 Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKG~~H~~PLTRRTKRS~~P~~QRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGT~~C~~QQP 300  
 W +W++ PPG+ AY C G C P  
 Sbjct: 316 GW-NDWIVAPPGYQAYYCHGEC~~P~~FP 339

tr Q8JFE2 Bmp4 protein [Bmp4] [Boulengerochromis microlepis (Giant cichlid)] 403 AA align

Score = 66.2 bits (160), Expect = 9e-10  
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE~~P~~VPKAALHRHGRLSPRSAQAR~~V~~TV-EWLRVRDDGSNRTS~~L~~IDS 165  
 +P + L A LRL++ + +A +S A R+ V E L+ G T L+D+  
 Sbjct: 145 IPED~~E~~LLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV~~L~~KAPRPGQLITQ~~L~~DT 201

Query: 166 RLVSVHESGWKA~~F~~DVTEAVNFXXXXXXV~~S~~VQREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +  
 Sbjct: 202 RLVRHN~~A~~RWESFDVSPAVLRW--TRERLPNYGLAVEVLH~~L~~NQT~~P~~RHQGRHVRISRSLHQ 259

Query: 226 APAGLGE~~P~~QLELHTLDLRDYGAQGDCDP-----EAPMTEGTR---CCRQEMYIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +  
 Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKG~~H~~PLTRRTKRS~~P~~QRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGT~~C~~QQP 300  
 W +W++ PPG+ AY C G C P  
 Sbjct: 316 GW-NDWIVAPPGYQAYYCHGEC~~P~~FP 339

tr Q8JIJ7 Bmp4 protein [Bmp4] [Julidochromis transcriptus] 403 AA align

Score = 65.9 bits (159), Expect = 1e-09  
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE~~P~~VPKAALHRHGRLSPRSAQAR~~V~~TV-EWLRVRDDGSNRTS~~L~~IDS 165  
 +P + L A LRL++ + +A +S A R+ V E L+ G T L+D+  
 Sbjct: 145 IPVDE~~E~~LLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV~~L~~KAPRPGQLITQ~~L~~DT 201

Query: 166 RLVSVHESGWKA~~F~~DVTEAVNFXXXXXXV~~S~~VQREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +  
 Sbjct: 202 RLVRHN~~A~~RWESFDVSPAVLRW--TRERLPNYGLAVEVLH~~L~~NQT~~P~~RHQGRHVRISRSLHQ 259

Query: 226 APAGLGE~~P~~QLELHTLDLRDYGAQGDCDP-----EAPMTEGTR---CCRQEMYIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +  
 Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKG~~H~~PLTRRTKRS~~P~~QRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWNVLEPPGFLAYECVGTQQP 300  
          W +W++ PPG+ AY C G C P  
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339

tr      [Q8JII3](#)      Bmp4 protein [Bmp4] [Tropheus duboisi]      403 AA  
align

Score = 65.5 bits (158), Expect = 1e-09  
Identities = 59/205 (28%), Positives = 87/205 (41%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGRLSPRSAQARVTW-EWLVRDDGSNRTSLIDS 165  
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+  
Sbjct: 145 IPEDELLSSAE LRLYRHOIDEAIADA--ISDDQALHRINVYEV LKAPRPGOLITOLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225  
           RLV       S W++FDV+ AV W                           V V + P G H + +  
 Sbjct: 202 RLVRHDASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHNOTPRHOGRHVRISRSLHO 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275  
           P      GE      +L    L  L   +G    G      P          +P      G      +      C  R      +Y+D   +  
 Sbjct: 260 EP---GEDWEOLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRAHALYVDFSDV 315

Query: 276 KWAKNWNVLEPPGFLAYECVGTCCQQP 300  
          W +W++ PPG+ AY C G C P  
Sbjct: 316 GW-NDWIVAAPPGYOOAYYCHGECPFP 339

tr Q90YJ3 Anti-dorsalizing morphogenetic protein [admp] [Brachydanio rerio (Zebrafish) (Danio rerio)] 391 AA align

Score = 65.1 bits (157), Expect = 2e-09  
Identities = 63/231 (27%), Positives = 92/231 (39%), Gaps = 63/231 (27%)

Query: 110 NSELVQAVLRLFQ-EPV ркаALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTS---LID 164  
 + +++ A L LF+ P L+RH V +V D G S L+  
 Sbjct: 118 SEKILTAELHLFKLRPKTSIVLNRRHFCO-----VS VY QVLD SGKK NVSO GK KLI S 168

Query: 165 SRLSVHESGWKAFDVTEAVNFXXXXXXXXXXXXVQREHLGPLAS----GAH--- 216  
SRLV +H +GW+ F +T+AV W +S + +LG L S G+  
Sbjct: 169 SRLVPIHSTGWEVFTITOAVRSW-----MSDEGSNLGLIVSVRTLAGSOMDI 215

Query: 217 KLVRFASQGAPAGLGE PQLELHTLD-----LRDYGAQGDCDPEAPMT----- 258  
           K+VRFAS                +P L L T D            L            D P +P  
 Sbjct: 216 KMVRFASGRDHHSKOPMLVLFDDGRRRAASI.EATSKGSDVS.PGSPSOSPL.PSV.PASRRSP 275

Query: 259 -----EGTRCCRQEMYIDLQGMWKAWNWVLEPPGFLAYECVGTQQP 300  
E C RQ +Y+D + + W+ W++ P G+ AY C G+C P  
Sbjct: 276 RSVVDYDERGEKMACOROPLIVDFFEEIGWS-GWIVSPKGYNAYHCKGSCIEP 325

tr Q8JIK0 Bmp4 protein [Bmp4] [Cyprichromis leptosoma] 403 AA

align

Score = 64.7 bits (156), Expect = 3e-09  
 Identities = 58/205 (28%), Positives = 87/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165  
 +P + L A LRL++ + +A +S R+ V E L+ G T L+D+  
 Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQXLH RINVYEVLKAPRPGQLITQLDT 201

Query: 166 RL VSVHESGWKA F D VTEAVNF WXXXXXXXXXXXXV SVQREHLGPLASGAHKLVRFASQG 225  
 RLV + S W++FDV+ AV W V V + P G H + +  
 Sbjct: 202 RL VRHN ASRWE SF DVSPAVLRW--TRERLPNYGLAVEVLH L NQT PRHQGQHVRISRSLHQ 259

Query: 226 APAGLGE P QLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275  
 P GE +L L L +G G P +P G + C R +Y+D +  
 Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRS PRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLE P P GFLAYECVGT CQQP 300  
 W +W++ PPG+ AY C G C P  
 Sbjct: 316 GW-NDWIVAPPGYQAYYCHGEC PFP 339

sp P21275 Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B) 408  
 BMP4\_MOUSE [Bmp4] [Mus AA  
 musculus (Mouse)] align

Score = 64.3 bits (155), Expect = 3e-09  
 Identities = 59/226 (26%), Positives = 87/226 (38%), Gaps = 32/226 (14%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQE PVPKA----ALRHGR LSPRSAQARVT 146  
 SE+S +F + +P N + A LRLF+E V + HR A +  
 Sbjct: 134 SESSAFRFLFNLS -IPENEVISSAELRLFRE QVDQGP DWEQGFHRINIYE VMKPPAEMV 192

Query: 147 VEWLVRDDGSNRTSLIDSRLVS VHESGWKA F D VTEAVNF WXXXXXXXXXXXXV SVQRE 206  
 G T L+D+RLV + + W+ FDV+ AV W + V  
 Sbjct: 193 -----PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREK QPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE----PQLEL-----HTLDLRDYGAQGDCDPE 254  
 H G H + S+ P G G+ P L HTL R P+  
 Sbjct: 243 HQTRTHQGQHVR I--SRSLPQGSGDWAQLRPLLVTFGHDGRGHTLRRRAKRS PKHH PQ 299

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWVLE P P GFLAYECVGT CQQP 300  
 + C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 300 RSRKKKNKNCRRHSL YVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344

tr Q8JIJ5 Bmp4 protein [Bmp4] [Oreochromis niloticus (Nile tilapia)] 403  
 (Tilapia AA  
 nilotica)] align

Score = 64.3 bits (155), Expect = 3e-09  
 Identities = 58/205 (28%), Positives = 87/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165  
 +P + L A LRL++ + +A +S R+ V E L+ G T L+D+

Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISHDQGLHRINVYEVLKAPRPGQLITQLLDT 201  
 Query: 166 RLVSVHESGWKA~~F~~DVTEAVNFXXXXXXVSVREHLGPLASGAHKLVRFASQG 225  
           RLV + S W++FDV+ AV W    V V + P G H + +  
 Sbjct: 202 RLVRHN~~A~~RWESFDVSPA~~V~~L~~R~~W--TRERLPNYGLAVEVLH~~L~~NQT~~P~~RHQGRHVRISRSLHQ 259  
 Query: 226 APAGLGE~~P~~QLELHTLDLRDYGAQGDCP-----EAPMTEGTR----CCRQEMYIDLQGM 275  
           P GE +L L L +G G P    +P G + C R +Y+D +  
 Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLRR~~T~~KRS~~P~~QRGRKRNRNCRRHALYVDFSDV 315  
 Query: 276 KWAKNWVLEPPGFLAYECVGT~~C~~QQP 300  
           W +W++ PPG+ AY C G C P  
 Sbjct: 316 GW-NDWIVAPPGYQAYYCHGEC~~P~~FP 339

tr Q8UVQ2 Anti-dorsalizing morphogenetic protein [admp] [Brachydanio rerio] (Zebrafish) (Danio rerio) 391 AA align

Score = 63.5 bits (153), Expect = 6e-09  
 Identities = 61/227 (26%), Positives = 91/227 (39%), Gaps = 55/227 (24%)

Query: 110 NSELVQAVLRLFQ-EPVPKAALHRHGRLSPRSAQARVTVEWLVRDDGSNRTSLIDSRLV 168  
       + +++ A L LF+ P L+RH Q V + + S L+ SRLV  
 Sbjct: 118 SEKILTAELH~~L~~FKL~~R~~PKTSIVLN~~R~~H----HFCQVS~~V~~YQVLDSSKKNVSQGKKLLSSRLV 172

Query: 169 SVHESGWKA~~F~~DVTEAVNFXXXXXXVSVREHLGPLAS-----GAH---KLVR 220  
       +H +GW+ F +T+AV W +S + +LG L S G+ K+VR  
 Sbjct: 173 PIHSTGWEVFTITQAVRSW-----MSDEGSNLGLLVSVRTL~~A~~GSQMDLK~~M~~VR 219

Query: 221 FASQGAPAGLGE~~P~~QLELHTLDLR-----DYGAQGDCDPEAPMTEGTR----- 262  
       FAS +P L L T D R D G P + R  
 Sbjct: 220 FASGRDH~~H~~HSKQPMLVLFTDDGRRAASLEATSKGSDVSPGGSSQPLPSVPASRRSSRSVD 279

Query: 263 -----CCRQEMYIDLQGMKWA~~N~~VLEPPGFLAYECVGT~~C~~QQP 300  
       C RQ +Y+D + + W+ W++ P G+ AY C G+C P  
 Sbjct: 280 YDERGEKMACQRQPLYVD~~E~~EIGWS-GWIVSPKGYNAYHCKGSCI~~F~~P 325

tr Q91597 Anti-dorsalizing morphogenetic protein 1 precursor [Xenopus laevis] (African clawed frog) 390 AA align

Score = 63.2 bits (152), Expect = 7e-09  
 Identities = 56/217 (25%), Positives = 86/217 (38%), Gaps = 38/217 (17%)

Query: 110 NSELVQAVLRLFQ---EPVPKAALHRHGRLSPRSAQARVTVEWLVRDDGSNRTSLIDS~~R~~ 166  
       N +++ A L LF+ P +A RH Q V + + + L+ S+  
 Sbjct: 120 NEKILTAELH~~L~~FKL~~R~~PK~~S~~EQAYFKRH----HFCQISVYMVL~~D~~KNKIQLPQGRKLLSSK 174

Query: 167 LVSVHESGWKA~~F~~DVTEAVNFXXXXXXVSVREHLGPLASGAHKLVRFASQGA 226  
       LV +H SGW+ F +T+AV W ++ + P ++RFAS  
 Sbjct: 175 LVPIHSSGWEVFSITQAVRAWNDESANHGILVTVRN~~L~~GGAQVDP-----NIIRFASGRD 228

Query: 227 PAGLGE~~P~~QLELHTLDLR---DYGAQGDCD-----PEAPMTEGTR-----C 263

+P L L T D R Q D P AP + TR C  
 Sbjct: 229 HHESKQPMVLFTDDGRRGIVSVNNQPDDQLMPLPNVPMAPTSNRTRLGRSVEEDGQLPC 288

Query: 264 CRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCCQQP 300  
 R +Y+D + + W+ W++ P G+ AY C G+C P  
 Sbjct: 289 QRHPLYVDFFEEIGWS-GWIISPRGYNAYHCKGSCPFP 324

tr Q8UVQ8 Anti-dorsalizing morphogenetic protein [admp] [Brachydanio rerio] (Zebrafish) (Danio rerio) 391 AA align

Score = 63.2 bits (152), Expect = 7e-09  
 Identities = 61/227 (26%), Positives = 91/227 (39%), Gaps = 55/227 (24%)

Query: 110 NSELVQAVLRLFQ-EPVPKAALHRHGRLSPRSAQARVTVEWLVRDDGSNRTSLIDSRLV 168  
 + + + A L LF+ P L+RH Q V + + S L+ SRLV  
 Sbjct: 118 SEKILTAELHLFKLRPKTSIVLNH----HFCQVSVYQVLDSKKNVSQGKKLLSSRLV 172

Query: 169 SVHESGWKA F D V T E A V N F W X X X X X X X X V S V Q R E H L G P L A S -----GAH---KLVR 220  
 +H +GW+ F +T+AV W +S + +LG L S G+ K+VR  
 Sbjct: 173 PIHSTGWEVFTITQAVRSW-----MSDEGSNLGLVSVRTL A G S Q M D L K M V R 219

Query: 221 FASQGAPAGLGE PQ LE LHTLDL R-----DYGAQGD C D P E A P M T E G T R ----- 262  
 FAS +P L L T D R D G P + R  
 Sbjct: 220 FASGRDHHSKQPMVLFTDDGRR A S L E A T S K G S D V S P G G X S Q P L P S V P A S R R S S R V D 279

Query: 263 -----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCCQQP 300  
 C R Q +Y+D + + W+ W++ P G+ A Y C G+C P  
 Sbjct: 280 YDERGEKMACQRQPLYVDFFEEIGWS-GWIIVSPKGYNAYHCKGSCIFP 325

tr Q8JIJ8 Bmp4 protein [Bmp4] [Haplochromis nyererei] 403 AA align

Score = 63.2 bits (152), Expect = 7e-09  
 Identities = 58/205 (28%), Positives = 87/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQE P VP KA AL HR HG RL SP RSA Q AR VT V -EW L VR DD G S N RT SL IDS 165  
 +P + L A L RL ++ + +A +S A R+ V E L+ G T L+ D+  
 Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQ LIT QLLDT 201

Query: 166 RL V SVHESGWKA F D V T E A V N F W X X X X X X X X V S V Q R E H L G P L A S G A H K L V R F A S Q G 225  
 R L V + S W++ F D V + A V W V V + P G H + +  
 Sbjct: 202 RL VRHN ASRWE SDV SPA VL RW --ARERLP NY GLA VE VL H L N Q T P R H Q G R H V R I S R S L H Q 259

Query: 226 A P A G L G E P Q L E L H T L D L R D Y G A Q G D -----CD P E A P M T E G T R -----CCRQEMYIDLQGM 275  
 P G E +L L L +G G +P G + C R +Y+D +  
 Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHSLTRRTKRS PRQR GRKR NRNC RR HALY VDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCCQQP 300  
 W +W++ P P G+ A Y C G C P  
 Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFP 339

tr Q811S3 Bone morphogenetic protein 4 [Bmp4] [Rattus norvegicus (Rat)] 408 AA

align

Score = 62.8 bits (151), Expect = 1e-08  
 Identities = 59/226 (26%), Positives = 85/226 (37%), Gaps = 32/226 (14%)

Query: 92 SEASTHLLVFGMEQRLLPPNSELVQAVLRLFQEPPVKA-----ALHRHGRLSPRSAQARVT 146  
 SE+S F + +P N + A LRLF+E V + HR A +  
 Sbjct: 134 SESSAFRFFFNLSS-IPENEVISSAELRLFREQVDQGPWEQGFHRINIVYEVMKPPAEMV 192

Query: 147 VEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFXXXXXXVSVQRE 206  
 G T L+D+RLV + + W+ FDV+ AV W + V  
 Sbjct: 193 -----PGHLITRLLDTRLVHNTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLG-----EPQLEL-----HTLDLIRDYGAQGDCDPE 254  
 H G H + S+ P G G P L HTL R P+  
 Sbjct: 243 HQTRTHQGQHVRI--SRSLPQSGGNWAQLRPLLVTFGHDGRGHTLRRRAKRSPKHHPO 299

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTQCP 300  
 + C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 300 RSRKKNNCRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344

tr Q6AYU9 Bmp4 protein [Bmp4] [Rattus norvegicus (Rat)] 408 AA

align

Score = 62.8 bits (151), Expect = 1e-08  
 Identities = 59/226 (26%), Positives = 85/226 (37%), Gaps = 32/226 (14%)

Query: 92 SEASTHLLVFGMEQRLLPPNSELVQAVLRLFQEPPVKA-----ALHRHGRLSPRSAQARVT 146  
 SE+S F + +P N + A LRLF+E V + HR A +  
 Sbjct: 134 SESSAFRFFFNLSS-IPENEVISSAELRLFREQVDQGPWEQGFHRINIVYEVMKPPAEMV 192

Query: 147 VEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFXXXXXXVSVQRE 206  
 G T L+D+RLV + + W+ FDV+ AV W + V  
 Sbjct: 193 -----PGHLITRLLDTRLVHNTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLG-----EPQLEL-----HTLDLIRDYGAQGDCDPE 254  
 H G H + S+ P G G P L HTL R P+  
 Sbjct: 243 HQTRTHQGQHVRI--SRSLPQSGGNWAQLRPLLVTFGHDGRGHTLRRRAKRSPKHHPO 299

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTQCP 300  
 + C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 300 RSRKKNNCRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344

tr Q8AYB5 Bone morphogenetic protein 4 (Fragment) [Oryzias latipes (Medaka fish) (Japanese ricefish)]

392  
AA  
align

Score = 62.0 bits (149), Expect = 2e-08  
 Identities = 58/216 (26%), Positives = 92/216 (41%), Gaps = 19/216 (8%)

Query: 95 STHLLVFGMEQRLPPNSELVQAVLRLFQE PVPKAALHRHGRLS PRSAQARVTVEWLVRD 154  
 S HL +P + L A LRL+++ +A + L+ + E L+  
 Sbjct: 133 SIHLRFLFNLSSIPEDELLSSAELRLYRQQLGEA--NDDSPNDQGLHRINIYEVLKPPR 190

Query: 155 DGSNRTSLIDSRLVS VHESGWKA F D VTEAVNF WXXXXXXXXXXXXV SVQRE H L G PL ASG 214  
 G T L+D+RLV + S W++FDV+ AV W ++V+ HL  
 Sbjct: 191 PGQLITQ LLDTRLVHHN ARWES FDV SPA VL RW----TRERLP NYGLA V E ILH L N QTPHN 246

Query: 215 AHKL VRFASQ GAPAGL GE PQ LE LHT L DLR DYGA QGD-----CDPEAPMTEGTR----CC 264  
 H+ VR S+ GE ++ L L +G G +P G + C  
 Sbjct: 247 QHRHVRI-SRSLHQEPGEDWDQVRPL-LVTFGHDGKGHS LTR RTKRSPKPRGRKRNRNCR 304

Query: 265 RQEM YIDLQGMKWA KNW VLEPPGFLAYECVGT CQQP 300  
 R +Y+D + W +W++ PPG+ AY C G C P  
 Sbjct: 305 RHTLYVDFSDVGW-NDWIVAPPGYQAYYCHGECPFP 339

tr P87380 Bone morphogenetic protein-4 (Fragment) [bmp4] [Brachydanio rerio (Zebrafish) (Danio rerio)] 391 AA align

Score = 61.6 bits (148), Expect = 2e-08  
 Identities = 48/163 (29%), Positives = 70/163 (42%), Gaps = 17/163 (10%)

Query: 148 EWLRVRDDGSNRTSLIDSRLVS VHESGWKA F D VTEAVNF WXXXXXXXXXXXXV SVQREH 207  
 E L+ +G T L+D+RLV + S W++FDV+ AV W V V +  
 Sbjct: 180 EVLKAPREGQ LITQ LLDTRLV RHNTSKWES FDV SPA VL RW--TQE KRSNH GLA VEV V QMK 237

Query: 208 LGPLASGAHKLVRFASQ GAPAGL GE PQ LE LHT L DLR DYGA QGD CDP-----EAPMTEGT 261  
 P+ G H V + P E +L L L +G G P +P G  
 Sbjct: 238 RNPVQKGRHVRVSR SVHPLP---DEEW DQLRPL-LVTFGHDGKSHPLTRRAKRS PKQRGR 293

Query: 262 R----CCRQEM YIDLQGMKWA KNW VLEPPGFLAYECVGT CQQP 300  
 + C R +Y+D + W +W++ PPG+ AY C G C P  
 Sbjct: 294 KRNRNCRRHALYVDFSDVGW-NDWIVAPPGYQAYYCHGECPFP 335

tr O57574 Bone genetic protein 4 (Hypothetical protein) (Bone morphogenetic protein 4) [bmp4] [Brachydanio rerio (Zebrafish) (Danio rerio)] 400 AA align

Score = 61.6 bits (148), Expect = 2e-08  
 Identities = 48/163 (29%), Positives = 70/163 (42%), Gaps = 17/163 (10%)

Query: 148 EWLRVRDDGSNRTSLIDSRLVS VHESGWKA F D VTEAVNF WXXXXXXXXXXXXV SVQREH 207  
 E L+ +G T L+D+RLV + S W++FDV+ AV W V V +  
 Sbjct: 181 EVLKAPREGQ LITQ LLDTRLV RHNTSKWES FDV SPA VL RW--TQE KRSNH GLA VEV V QMK 238

Query: 208 LGPLASGAHKLVRFASQ GAPAGL GE PQ LE LHT L DLR DYGA QGD CDP-----EAPMTEGT 261  
 P+ G H V + P E +L L L +G G P +P G  
 Sbjct: 239 RNPVQKGRHVRVSR SVHPLP---DEEW DQLRPL-LVTFGHDGKSHPLTRRAKRS PKQRGR 294

Query: 262 R----CCRQEM YIDLQGMKWA KNW VLEPPGFLAYECVGT CQQP 300  
 + C R +Y+D + W +W++ PPG+ AY C G C P

Sbjct: 295 KRNRNCRRHALYVDFSDVGW-NDWIVAPPGYQAYYCHGECPFP 336

tr Q6J3S5 Bone morphogenetic protein 24B [BMP24B] [Petromyzon marinus] 451  
 (Sea  
 lamprey) ] AA align

Score = 61.2 bits (147), Expect = 3e-08  
 Identities = 67/287 (23%), Positives = 109/287 (37%), Gaps = 33/287 (11%)

Query: 45 RADMEKLV---IPAHVRAQYVVLRRSHGDRS--RGKRFQSFSREVAGRFLASEASTHLL 99  
 RAD E++ + V R + G + RG +S +++ + T

Sbjct: 103 RADKERVGKDDVDVEEEKEEVAFPREAQGRANTVRGFHHDESTEKLSLGQSTEDGTTWHF 162

Query: 100 VFGMЕQRLPPNSELVQAVLRLFQE PV--PKAALHRHGR LSPRSAQARVTVEWLRVRDDGS 157  
 +F + +P + E+ A LR+ V P + L+PR + V

Sbjct: 163 LFNLSS-IPDSEEVTAELRVHHTRVHSPCPSSPACE LAPRLERINVYEVVAPPSSPSG 221

Query: 158 NRTSLIDSRLVSVHESGWKA F DVTEAVNFWXXXXXXXXXXXXX-SVQREHLGPLASGAH 216  
 + L+D+R+V +ES W+AFDV+ AV+ W V V+R G A+G

Sbjct: 222 AASRLLLDTRVVRTNESRWEAFDVSPAVSRWTRGSAPNRGFAVEVLPVRRPSGGVAANGVP 281

Query: 217 KLVRFASQGAPAGLGE P QLELHTLDLRDYGAQGDCDP EAPMTEGTR----- 262  
 A + P H + R D AP T +R

Sbjct: 282 SEAVLAQPRSGVASLFPGDGSHQTEPRPLLVTFGSDGRAPTPRSRARRSIGGAPRQAAH 341

Query: 263 -----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQP 300  
 C R +Y+D + + W +W++ PPG+ AY C G C P

Sbjct: 342 KARRKPRYSCR RHALYVDFREV GW-NDWIVAPPGYHAYFCHGECPFP 387

tr O13107 BMP4 [bmp4] [Brachydanio rerio (Zebrafish) (Danio rerio)] 400 AA

align

Score = 60.8 bits (146), Expect = 4e-08  
 Identities = 47/163 (28%), Positives = 69/163 (41%), Gaps = 17/163 (10%)

Query: 148 EWLRVRDDGSNRTSLIDSRLVSVHESGWKA F DVTEAVNFWXXXXXXXXXXXXVSVQREH 207  
 E L+ +G T L+D+RLV + S W++FDV+ AV W V V +

Sbjct: 181 EVLKAPREGQLITQLLDTRLVRPNNTSKWESFDVSPAVLRW--TQEKR SNHGLAVEVVQMK 238

Query: 208 LGPLASGAHKLVRFASQGAPAGLGE P QLELHTLDLRDYGAQGDCDP-----EAPMTEGT 261  
 P+ G H V + P E + L L +G G P +P G

Sbjct: 239 RNPVQKGRHARVSRSVHPLP---NEEWDHVRPL-LVTFGHDGKSHPLTRRAKRS PKQRGR 294

Query: 262 R----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQP 300  
 + C R +Y+D + W +W++ PPG+ AY C G C P

Sbjct: 295 KRNRNCRRHALYVDFSDVGW-NDWIVAPPGYQAYYCHGECPFP 336

tr Q9XYQ8 Bone morphogenetic protein BMP2/4 (Fragment) [BMP2/4] 289 AA  
 [Strongylocentrotus purpuratus (Purple sea urchin)] align

Score = 60.8 bits (146), Expect = 4e-08  
 Identities = 57/222 (25%), Positives = 88/222 (38%), Gaps = 34/222 (15%)

Query: 107 LPPNSELVQAVLRLFQEP-----VPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRT 160  
 +P + A LRLF++ V + ALH L P R+ V + ++ NR  
 Sbjct: 7 MPEEEVMTTAELRLFRKDLDEHHIVKRHALHDRESLKPIHYMQRINVYHI-LKPVARNRD 65

Query: 161 S---LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXVSVQREHLGPLASGAHK 217  
 + LID+RLV V + W++FDV A+ W + R P H  
 Sbjct: 66 TIKRLIDTRLVDVRNASWESFDVRPAMRVWLEEPEKNHGLEIELIDSRGRRPSP---NHH 121

Query: 218 LVRFASQGAPAGLGE-----PQLELHTLDLRYGAQGDCDP--EAPMTEGTR 262  
 VR + P+ + E PQ+ ++ D R + +G R  
 Sbjct: 122 HVRVTREADPSKVEELENNEEDRWFQTRPQIVTYSDDGRTKRSPPSSSSGRGQKKRKKGKR 181

Query: 263 ----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTQQP 300  
 C R E+Y+D + W +W++ P G+ AY C G C P  
 Sbjct: 182 LKANCRRELVDFSDVHW-NDWIVAPAGYQAYYCRGECPPFP 222

sp Q90752 **Bone morphogenetic protein 4 precursor (BMP-4) [BMP4]** 405  
BMP4\_CHICK **[Gallus** AA  
**gallus (Chicken)]** align

Score = 60.5 bits (145), Expect = 5e-08  
 Identities = 62/224 (27%), Positives = 93/224 (40%), Gaps = 31/224 (13%)

Query: 92 SEASTHLLVFGMEOQLPPNSELVQAVLRLFQE PV--PKAALHRHGRLSPRSAQARVT-E 148  
 SEA VF + +P N + LRL+E V P AA R R+ + E  
 Sbjct: 134 SEAPRIRFVFNLSS-VPDNEVISSEELRLYREQVEEPSAAWERGFH-----RINIYE 184

Query: 149 WLVRRDDGSNR-TSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXVSVQREH 207  
 ++ + S T L+D+RLV + + W+ FDV+ AV W + V H  
 Sbjct: 185 VMKPLSERSQAITRLLDTRLVHHNVTRWETFDVSPAIVRW--TKDKQPNHGLVIEVTHLH 242

Query: 208 LGPLASGAHKLVRFASQGAPAGLGE PQLELHTLDLRYGAQGDCDP-----EAPMTEGT 261  
 G H + S+ P G G +L L L +G G +P G+  
 Sbjct: 243 QAOTHQGKHVRI--SRSLPQGHGGDWQLRPL-LVTFGHDGRGHALTRARRSPKHHGS 298

Query: 262 R-----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTQQP 300  
 R C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 299 RKNKKNCRRHALYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPPFP 341

sp P25703 **Bone morphogenetic protein 2-I precursor (BMP-2-I)** 398  
BMPA\_XENLA **[Xenopus laevis** AA  
**(African clawed frog)]** align

Score = 59.3 bits (142), Expect = 1e-07  
 Identities = 59/210 (28%), Positives = 89/210 (42%), Gaps = 35/210 (16%)

Query: 109 PNSELV-QAVLRLFQE PVPK-----AALHR---HGRLSPRSAQARVTVEWLRVRDDGSN 158  
 PN ELV A LR+F+E V + + LHR + + P+A +R V  
 Sbjct: 142 PNEELVTSaelrifreqvqepfesdssklhriniydivkpaaaasrgpv----- 190

Query: 159 RTSLIDSRLVSVHESGWKA F D V T E A V N F W X X X X X X X X V S V Q R E H L G P L A S G A H K L 218  
           L+D+RLV +ES W++FDVT A+ W V+ HL + K  
 Sbjct: 191 -V R L L D T R L V H H N E S K W E S F D V T P A I A R W I A H K Q P N H G F V --- V E V N H L D N D K N V P K K H 245

Query: 219 V R F A S Q G A P A G L G E P Q --- L E L H T L D L R D Y G A Q G D C D P E A P M T E G T R --- C C R Q E M Y I 270  
           V R + P P Q L + D + + + A + R C R + Y +  
 Sbjct: 246 V R I S R S L T P D K D N W P Q I R P L L V T F S H D G K G H A L H K R Q K R Q A R H K Q R K R L K S S C R R H P L Y V 305

Query: 271 D L Q G M K W A K N W V L E P P G F L A Y E C V G T C Q Q P 300  
           D + W +W++ P P G + A+ C G C P  
 Sbjct: 306 D F S D V G W -N D W I V A P P G Y H A F Y C H G E C P F P 334

tr Q8MJV5 Bone morphogenetic protein 4 [sBmp4] [Suncus murinus (House shrew) (Mus shrew)] 409 AA align

Score = 58.5 bits (140), Expect = 2e-07  
 Identities = 58/227 (25%), Positives = 84/227 (36%), Gaps = 33/227 (14%)

Query: 92 S E A S T H L L V F G M E Q R L P P N S E L V Q A V L R L F Q E P V P K A --- A L H R H G R L S P R S A Q A R V T 146  
           S E S F + + P N + A L R L F + E V + H R A V  
 Sbjct: 134 S E N S A F R F F F N L S S -I P E N E V I S S A E L R L F R E Q V D Q G P D W E Q G F H R I N I Y E V M K P P A E V V 192

Query: 147 V E W L R V R D D G S N R T S L I D S R L V S V H E S G W K A F D V T E A V N F W X X X X X X X X V S V Q R E 206  
           G T L+D+RLV + + W+ FDV+ AV W + V  
 Sbjct: 193 -----P G H L I T R L L D T R L V H H N V T R W E T F D V S P A V L R W --T R E K Q P N Y G L A I E V T H L 242

Query: 207 H L G P L A S G A H K L V R F A S Q G A P A G L G E -----P Q L E L H T L D L R D Y G -----A Q G D C D P 253  
           H G H + S+ P G G+ P L D R + P  
 Sbjct: 243 H Q T R T H Q G Q H V R I --S R S L P Q G N G D W A Q L R P L L V T F G H D G R G H A L T R R R R A K R S P K H H P 299

Query: 254 E A P M T E G T R C C R Q E M Y I D L Q G M K W A K N W V L E P P G F L A Y E C V G T C Q Q P 300  
           + + C R +Y+D + W +W++ P P G + A+ C G C P  
 Sbjct: 300 Q R A R K K N K N C R R H S L Y V D F S D V G W -N D W I V A P P G Y Q A F Y C H G D C P F P 345

sp P49001 Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A) 393  
 BMP2\_RAT [Bmp2]  
 [Rattus norvegicus (Rat)] AA align

Score = 57.4 bits (137), Expect = 4e-07  
 Identities = 54/211 (25%), Positives = 89/211 (41%), Gaps = 35/211 (16%)

Query: 107 L P P N S E L V Q A V L R L F Q E P V P K A A L H R H G R L S P R S A Q A R V T V E W L R V R D D G S N R --T S L I 163  
           + P + L A L++F+E + + A L S Q R + . + S++ T L+  
 Sbjct: 137 V P T D E F L T S A E L Q I F R E Q M Q E A -----L G N S S F Q H R I N I Y E I I K P A T A S S K F P V T R L L 189

Query: 164 D S R L V S V H E S G W K A F D V T E A V N F W X X X X X X X X V S -----V Q R E H L G P L A S G A H 216  
           D+RLV+ + S W++FDVT AV W V+ V + H+ ++ H  
 Sbjct: 190 D T R L V T Q N T S Q W E S F D V T P A V M R W T A Q G H T N H G F V V E V A H L E E K P G V S K R H V -R I S R S L H 248

Query: 217 K L V R F A S Q G A P A -----G L G E P Q L E L H T L D L R D Y G A Q G D C D P E A P M T E G T R C C R Q E M Y 269  
           + S Q P G G P L H + R + + C R + Y  
 Sbjct: 249 Q D E H S W S Q V R P L L V T F G H D G K G H P --L H K R E K R -----Q A K H K Q R K R L K S S C R H P L Y 299

Query: 270 IDLQGMKWA  
N WVLEPPGFLAYECVGT  
CQQP 300  
+D + W +W++ PPG+ A+ C G C P  
Sbjct: 300 VDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 329

sp P21274 **Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A)** 394  
BMP2\_MOUSE [Bmp2] [Mus  
musculus (Mouse)] AA  
align

Score = 57.4 bits (137), Expect = 4e-07  
Identities = 54/211 (25%), Positives = 89/211 (41%), Gaps = 35/211 (16%)

Query: 107 LPPNSELVQAVLRLFQE  
PVPKAALHRHGR  
LS PRSAQARVT  
VEWLVRDDGSNR---TSL 162  
+P + L A L++F+E + +A L S Q R+ + ++ +N T L  
Sbjct: 138 VPSDEF  
LTS AELQI FREQ  
I QEA-----LGNSSFQH  
RINIYEI-IKPAAANL  
KFVTRL 189

Query: 163 IDSRLVSVHESGW  
KAFDVTEAVNF  
WXXXXXXXXXXXX  
VSVQREHLG----PLASGAH 216  
+D+RLV+ + S W++FDVT AV W V+ E+ G ++ H  
Sbjct: 190 LDTRLV  
NQNTSQWE  
SF DVT  
PAVMRWTTQGHT  
NHGFVVEVAH  
LEENPGVSKR  
HVRI  
S LH 249

Query: 217 KLVRFASQGAPA-----GLGE  
PQLELHTLDLRDYGA  
QGD  
CDPEAPMTEGTRCC  
RQEMY 269  
+ SQ P G G P LH + R + + C R + Y  
Sbjct: 250 QDEHSWSQIRPLL  
VTFGHDGKGHP--LHKREKR-----QAKHKQR  
KRLKSSCKRHPLY 300

Query: 270 IDLQGMKWA  
N WVLEPPGFLAYECVGT  
CQQP 300  
+D + W +W++ PPG+ A+ C G C P  
Sbjct: 301 VDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 330

tr Q90YD7 **Bone morphogenetic protein 2 (BMP-2) [BMP-2] [Xenopus  
tropicalis  
(Western clawed frog) (Silurana tropicalis)]** 398  
AA  
align

Score = 57.4 bits (137), Expect = 4e-07  
Identities = 57/210 (27%), Positives = 88/210 (41%), Gaps = 35/210 (16%)

Query: 109 PNSELV-QAVLRLFQE  
PVPK-----AALHR---HGR  
LSPRS  
AQARVT  
VEWLVRDDGSN 158  
PN ELV A LR+F+E V + + LHR + + P +A +R V  
Sbjct: 142 PNEELV  
TSAELRIFREGV  
QE PFE  
GDSSKLHR  
INIYDIV  
VKPAAA  
SRGPV----- 190

Query: 159 RTSLIDSRLV  
SVHESGW  
KAFDVTEAVNF  
WXXXXXXXXXXXX  
VSVQREHLG  
PLASGAHKL 218  
L+D+RL+ +ES W++FDVT A+ W V+ HL + K  
Sbjct: 191 -VRLLD  
TRLIH  
HNE SKW  
EFDVTPA  
ITRWI  
AHKQPNH  
GFVVEVT---HLDND  
KNVPKKH 245

Query: 219 VRFASQGAPAGLG---EPQLE  
LHTLDLRDYGA  
QGD  
CDPEAPMTEGTR---CCRQEMYI 270  
VR + P P L + D + + +A + R C R + Y+  
Sbjct: 246 VRISRS  
LVPDKDSW  
PRIRPL  
LVTFSHDGKG  
HALHKREK  
RQARHKQR  
KRLKSSCRRH  
PLYV 305

Query: 271 DLQGMKWA  
N WVLEPPGFLAYECVGT  
CQQP 300  
D + W +W++ PPG+ A+ C G C P  
Sbjct: 306 DFSDVGW-NDWIVAPPGYHAFYCHGECPFP 334

tr Q90YD6 Bone morphogenetic protein 4 [BMP-4] [Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)] 400 AA align

Score = 57.4 bits (137), Expect = 4e-07  
 Identities = 49/220 (22%), Positives = 90/220 (40%), Gaps = 24/220 (10%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQE PVPKAALHRHG--RLSPRSAQARVTVEW 149  
 +E VF + +P N + A LRL++E + G R++ +T  
 Sbjct: 130 AENGNFRFVFNLS -IPENEVISSAELRLYREQIDHGP AWEEGFHRINIYEVMKPI TAS- 187

Query: 150 LRVRDDGSNRTSLIDSRLVSVHESGWKA F DVTEAVNFWXXXXXXXXXXXXVSVQREHLG 209  
 G + L+D+RL+ + + W++FDV+ A+ W +++++ HL  
 Sbjct: 188 -----GHMISRLLDTRLIHHNVTQWE SFDV SPAIRWTRDKQINHG---LAIEVVHLN 237

Query: 210 PLASGAHKLVRFASQGAPAGLGE----PQLELHTLDLRDYG---AQGDCDPEAPMTEG 260  
 + K VR + P + P L + D R + ++ + P +  
 Sbjct: 238 QTKTYQGKHVRISRSLLPQEDADWSQMRPLLITFSHDGRGH ALTRRSKRSPKQQRPRKKN 297

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQP 300  
 C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 298 KHCCRHS LYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 336

tr Q6PAF3 LOC397874 protein [LOC397874] [Xenopus laevis (African clawed frog)] 400 AA align

Score = 56.6 bits (135), Expect = 7e-07  
 Identities = 50/220 (22%), Positives = 91/220 (40%), Gaps = 24/220 (10%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQE PVPKAALHRHG--RLSPRSAQARVTVEW 149  
 +E VF + +P N + A LRL++E + G R++ +  
 Sbjct: 130 AENGNFRFVFNLS -IPENEVISSAELRLYREQIDHGP AWEGFHRINIYEVMKPIAANG 188

Query: 150 LRVRDDGSNRTSLIDSRLVSVHESGWKA F DVTEAVNFWXXXXXXXXXXXXVSVQREHLG 209  
 L + NR L+D+RL+ + + W++FDV+ A+ W +++++ HL  
 Sbjct: 189 LMI-----NR--LLDTRLIHHNVTQWE SFDV SPAIMRWTRDKQINHG---LAIEVIHLN 237

Query: 210 PLASGAHKLVRFASQGAPAGLGE----PQLELHTLDLRDYG---AQGDCDPEAPMTEG 260  
 + K VR + P + P L + D R + ++ + P +  
 Sbjct: 238 QTKTHQGKHVRISRSLLPQEDADWSQMRPLLITFSHDGRGH ALTRRSKRSPKQQRPRKKN 297

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQP 300  
 C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 298 KHCCRHS LYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 336

tr Q91703 Bone morphogenetic protein 4 [BMP-4] [Xenopus laevis (African clawed frog)] 400 AA align

Score = 56.6 bits (135), Expect = 7e-07  
 Identities = 50/220 (22%), Positives = 91/220 (40%), Gaps = 24/220 (10%)

Query: 92 SEASTHLLVFGMEQLPPNSELVQAVLRLFQE PVPKA ALHRHG--RLSPRSAQARVTVEW 149  
 +E VF + +P N + A LRL+E + G R++ +  
 Sbjct: 130 AENGNFRFVFNLSS-IPENEVISSAELRLYREQIDHGP AWDEGFHRINIYEVMKPIAANG 188

Query: 150 LRVRDDGSNRTSLIDSRLVS VHESGWKA F D VTEAVNFWXXXXXXXXXSVQREHLG 209  
 L + NR L+D+RL+ + W++FDV+ A+ W +++++ HL  
 Sbjct: 189 LMI----NR--LLDTRLIHVN T QWE SFDV SPAIMRWT RDQINHG---LAIEVIHLN 237

Query: 210 PLASGAHKLVRFASQGAPAGLGE----PQLELHTLDLRDYG----AQGDCDPEAPMTEG 260  
 + K VR + P + P L + D R + ++ + P +  
 Sbjct: 238 QTKTHQGKHVRISRSLLPQEDADWSQMRPLLITFS HDGRGH ALTRRSKRSPKQQRPRKKN 297

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQP 300  
 C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 298 KHCCRHS LYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 336

tr Q9MZV5 Bone morphogenetic protein 4 (Fragment) [bmp4] [Canis familiaris (Dog)] 337  
 AA align

Score = 56.6 bits (135), Expect = 7e-07  
 Identities = 58/227 (25%), Positives = 85/227 (36%), Gaps = 33/227 (14%)

Query: 92 SEASTHLLVFGMEQLPPNSELVQAVLRLFQE PVPK----AALRHGRLSPRSAQARVT 146  
 SE S +F + +P N + A LRL+E V + HR A V  
 Sbjct: 62 SENSAFRFLFNLS S-IPENEVISSAELRLFREQVNQDPDWEQGFHRINIYEVMKPPAEVV 120

Query: 147 VEWLVRDDGSNRTSLIDSRLVS VHESGWKA F D VTEAVNFWXXXXXXXXXSVQRE 206  
 G T L+D+RLV + + W+ FDV+ AV W + V  
 Sbjct: 121 -----PGHLITRLLDTRLVHHNVTRWETFDV SPAVL RW--TREKQPNYGLAIEVTHL 170

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE----PQLEL-----HTLDLRDYGAQG-DCDP 253  
 H G H + S+ P G G+ P L H L R +  
 Sbjct: 171 HQTRTHQGQHVRI--SRSLPQGSGDWAQLRPLLVTFGHDGRGH ALTRRQRAKRS PKHHA 227

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQP 300  
 + + C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 228 QRARKKNKNCRHSL YVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 273

sp P12644 Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B) 408  
 BMP4\_HUMAN [BMP4] AA align  
 [Homo sapiens (Human)]

Score = 56.2 bits (134), Expect = 9e-07  
 Identities = 58/227 (25%), Positives = 85/227 (36%), Gaps = 33/227 (14%)

Query: 92 SEASTHLLVFGMEQLPPNSELVQAVLRLFQE PVPK----ALRHGRLSPRSAQARVT 146  
 SE S +F + +P N + A LRL+E V + HR A V  
 Sbjct: 133 SENSAFRFLFNLS S-IPENEVISSAELRLFREQV DQGP DWERGFHRINIYEVMKPPAEVV 191

Query: 147 VEWLVRDDGSNRTSLIDSRLVS VHESGWKA F D VTEAVNFWXXXXXXXXXSVQRE 206  
 G T L+D+RLV + + W+ FDV+ AV W + V  
 Sbjct: 192 -----PGHLITRLLDTRLVHHNVTRWETFDV SPAVL RW--TREKQPNYGLAIEVTHL 241

Query: 207 HLGPLASGAHKLVRFASQGAPAGLG-----EPQLELHTLDLRDYG---AQGDCDP---- 253  
 H G H + S+ P G G P L D R + + P  
 Sbjct: 242 HQTRTHQGQHVRI---SRSLPQGSGNWAQLRPLLVTFGHDGRGHALTRRRRAKRSPKHHS 298

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCCQP 300  
 + + C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 299 QRARKKNNKNCRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344

tr Q6J3S6 Bone morphogenetic protein 24A [BMP24A] [Petromyzon marinus 422  
 (Sea AA  
 lamprey)] align

Score = 56.2 bits (134), Expect = 9e-07  
 Identities = 81/291 (27%), Positives = 114/291 (38%), Gaps = 50/291 (17%)

Query: 54 PAHVRAQYVVLLRRS-HGDRSRGKRFQSFSREVAGRFLASEASTHLLVFGME--QRLPPN 110  
 P V Y++ L R+ HG S + + + R AS+A+T E + +P +  
 Sbjct: 74 PGAVVPPYMLQLYRALHGAHSGARDVGRPLDRLVAR-PASQANTVRSFHHDSEAHVPAD 132

Query: 111 SELVQAVLRLFQ-----EPVPKAALH--RHGRRLSPRSAQA-RVTV-EWLR-VRDDGSN 158  
 S A LF E + A LH R SP SA R+ V E LR DG+  
 Sbjct: 133 SGDSTARLLFNVSSIPDGEVITSAELHVYRERLSSPASAGLHRINVYEVLRPAAADGTP 192

Query: 159 RTSLIDSRLVSVHESGWKAFFDVTEAVNFXXXXXXXXXXXXVSVQREHLGPLASGAHKL 218  
 L+D+R+V S W+ FDV+ A W + V+ +HL +  
 Sbjct: 193 IARLLDTRVVHSGRSEWERFDVSPAARWAATKEPNHG---LLVEVQHLDGGTPEKRRH 248

Query: 219 VRF-----ASQGAPAGLGE P Q L E -----HTLDLRDYGAQGDCDPEA- 255  
 VR AS+G G G P Q L H RD G P+  
 Sbjct: 249 VRIGRSLHAEAVAAAARDGASEGGDGEGWPQLRPLLVTFGHDGKTRDEGTLLRPRPKRN 308

Query: 256 --PMTEGTR---CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCCQP 300  
 P G R C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 309 SRPNKGRRGRGQCARYPLYVDFSDVGW-NDWIVAPPGYNAFFCQGECHFP 358

tr O73818 Bone morphogenetic protein 4 [BMP-4] [Xenopus laevis (African 400 AA clawed frog)] align

Score = 56.2 bits (134), Expect = 9e-07  
 Identities = 47/205 (22%), Positives = 86/205 (41%), Gaps = 23/205 (11%)

Query: 107 LPPNSELVQAVLRLFQE P VP KAALHRHG--RLSPRSAQARVTVEWLVRVDDGSNRTSLID 164  
 +P N + A LRL++E + G R++ + L + NR L+D  
 Sbjct: 144 IPENEVISSAELRLYREQIDHGP AWDEGFHRINIYEV MKPIAANGLMI----NR--LLD 196

Query: 165 SRLVSVHESGWKAFFDVTEAVNFXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQ 224  
 +RL+ + + W++FDV+ A+ W +++++ HL + K VR +  
 Sbjct: 197 TRLIHHNVTQWESFDVSPAIMRWTRDKQINHG---LAIEVIHLNQT KTHQGKHVRISRS 252

Query: 225 GAPAGLGE-----P Q L E H T L D L R D Y G ---AQGDCDPEA P M T E G T R C C R Q E M Y I D L Q G M 275  
 P + P L + D R + ++ + P + C R +Y+D +

Sbjct: 253 LLPQEDADWSQMRPLLITFSHDGRGHALTRRSKRSPQQPRKKNKHCRHSLYVDFSDV 312

Query: 276 KWAKNWVLEPPGFLAYECVGTQQP 300

W +W++ PPG+ A+ C G C P

Sbjct: 313 GW-NDWIVAPPGYQAFYCHGDCPFP 336

tr Q9U418 Bone morphogenetic protein 2/4 [BMP2/4] [Branchiostoma belcheri (Amphioxius)] 411 AA align

Score = 55.8 bits (133), Expect = 1e-06

Identities = 54/206 (26%), Positives = 83/206 (40%), Gaps = 18/206 (8%)

Query: 109 PNSELVQAV-LRLFQE PVPKAALHRHGRLSPRSAQARVTVEWLRV--RDDGSNRTSLIDS 165  
P+ EL++A LRLF+E + + ++G + E +R R + T L+D+

Sbjct: 145 PSVELIKAELRLFREQIDVDHV-QYGDSTDHHLYRVNVYEVMPNSRTNTDTITRLDT 203

Query: 166 RLVS VHESGWKA FDVTEAVNFWXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225  
+LV V S W++FDV AV W V V G L++ +L R

Sbjct: 204 KLVDVRNSSWESFDVRSAVTKWKNSPERNYGLE--VEVVSPKRGALSNNHVRLLRSTDMD 261

Query: 226 APAGLGE-PQLELHTLDLRDYGAQGDCDPEAPMTEGTR-----CCRQEMYIDLQG 274  
A P L +T D + G + C R +Y+D

Sbjct: 262 DHAWQHRRPPLLTYTDDKGSSNSNRVASRQKRANGRKHHQRRRLKANCRHSLYVDFSD 321

Query: 275 MKWAKNWVLEPPGFLAYECVGTQQP 300

+ W +W++ PPG+ AY C G C P

Sbjct: 322 VGW-NDWIVAPPGYQAYYCHGECPFP 346

sp O46576 Bone morphogenetic protein 4 precursor (BMP-4) [BMP4] 409  
BMP4\_RABBIT [Oryctolagus cuniculus (Rabbit)] AA align

Score = 55.5 bits (132), Expect = 2e-06

Identities = 58/224 (25%), Positives = 84/224 (36%), Gaps = 27/224 (12%)

Query: 92 SEASTHLLVFGMEQRLLPPNSELVQAVLRLFQE PVPKA----ALHRHGRLSPRSAQARVT 146  
SE S +F + +P N + A LRLF+E V + HR A

Sbjct: 134 SENSAFRFLFNLS-IPENEAISSAELRLFREQDQGPDWERGFHRINIYEVMKPPAEAV 192

Query: 147 VEWLVRDDGSNRTSLIDSRLVS VHESGWKA FDVTEAVNFWXXXXXXXXXXXXVSVQRE 206  
G T L+D+RLV + + W+ FDV+ AV W V V

Sbjct: 193 -----PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNHGLAVEVTHF 242

Query: 207 HLGPLASGAH-KLVRFASQGAPAGLGE PQLEL-----HTLDLRDYGAQG-DCDPEAP 256  
H G H +L R QG+ L + H L R + P+

Sbjct: 243 HHTRTHQGHVRLSRSLLQGSGDWAQFRPLLVTFGHDGRGHALTRRRRAKRSLKHHHQRA 302

Query: 257 MTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTQQP 300

+ C R +Y+D + W +W++ PPG+ A+ C G C P

Sbjct: 303 RKKNKNCRRAHALYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 345

tr Q90Y82 LjBmp2/4a (Fragment) [LjBmp2/4a] [Lampetra japonica (Japanese lamprey) (Entosphenus japonicus)]

align

Score = 55.1 bits (131), Expect = 2e-06  
 Identities = 59/229 (25%), Positives = 87/229 (37%), Gaps = 53/229 (23%)

Query: 107 LPPNSELVQAVLRLFQE PVP---KAALHR---HGRRLSPRSAQARVTVEWLRVRDDGSNRT 160  
 +P + A L +++E + +AALHR + L P +A DG+  
 Sbjct: 3 IPDGEVITS AELHVY RERL SGPARA ALHR INVY EVLR PAAA-----DGTPIA 49

Query: 161 SLIDSRLV SVHESGWKA F D VTEAVNFW XXXXXXXXXX VSQREHLGPLASGAHKLVR 220  
 L+D+R+V S W+ FDV+ A W + V+ HL + VR  
 Sbjct: 50 RLLDTRVVHSGRSEWERFDVSPAAVRWAARAPNHG---LLVEVHLDGGTPEKRRHVR 105

Query: 221 F-----ASQGAPAGLGE P Q L E-----HTLDL RDYGAQGD C D PEA--- 255  
 A + G G G P Q L H RD G P+  
 Sbjct: 106 IGRSLHAE AVAAAARDGAGEGGDGGE GPQLRPLLVTFGHDGKTRDEGTLLRPRPKNSR 165

Query: 256 PMTEGTR----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300  
 P G R C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 166 PNKGGR RGRGQCARYPLYVDFSDVGW-NDWIVAPPGYNAFFCQGECHFP 213

tr O96504 Bone morphogenetic protein 2/4 [AmphiBMP2/4] [Branchiostoma 361 AA floridae (Florida lancelet) (Amphioxus)]

align

Score = 55.1 bits (131), Expect = 2e-06  
 Identities = 53/205 (25%), Positives = 83/205 (39%), Gaps = 17/205 (8%)

Query: 109 PNSELVQAV-LRLFQE P VP KAALHR HGRRLSPRSAQARVTVEWLRV--RDDGSNRTS LIDS 165  
 P+ EL++A LRLF+E + + ++G + E +R R + T L+D+  
 Sbjct: 96 PSVELIKA AE LRLFREQ IDVDHV-QYGDSTDHHLYRVNVYEVMRPNSRTNTDTITRLLDT 154

Query: 166 RL VSVHESGWKA F DVTEAVNFW XXXXXXXXXX VSQREHLGPLASGAHKLVR FASQG 225  
 +LV V S W++FDV AV W V V G L++ +L R  
 Sbjct: 155 KLV D VRN SSWESFDV RSAVTKWKN SPERNYGLE--VEVVSPKR GALS NHV RL RR STDMD 212

Query: 226 APAGLGE-P Q L E H T L D L R D Y G A Q G D C D P E A P M T E G T R -----CCRQEMYIDLQGM 275  
 + P L +T D + G + C R +Y+D +  
 Sbjct: 213 DHSWQHRRP L L T Y T D D G K G S S N S R V A S R Q K R A N G R K K Q R R R L K A N C R R H S L Y V D F S D V 272

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300  
 W +W++ PPG+ AY C G C P  
 Sbjct: 273 GW-NDWIVAPPGYQAYYCHGEC PFP 296

sp Q29607 Bone morphogenetic protein 4 precursor (BMP-4) [BMP4] 408  
 BMP4\_DAMDA [Dama dama] AA  
 (Fallow deer) (Cervus dama)] align

Score = 54.3 bits (129), Expect = 3e-06  
 Identities = 56/227 (24%), Positives = 83/227 (35%), Gaps = 34/227 (14%)

Query: 92 SEASTHLLVFGMEQLPPNSELVQAVLRLFQE PVPKA-----ALHRHGRLSPRSAQARVT 146  
 SE S +F + +P N + A LR F+E V + HR A  
 Sbjct: 134 SENSAFRFLFNLS--IPENQVISTAEELRDFREQVDQGPDWERGFHRINIYEVMKPPAEAV 191

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKA FDVTEAVNFWXXXXXXXXXXXXVSVQRE 206  
 G T L+D+RLV + + W+ FDV+ AV W + V  
 Sbjct: 192 -----PGHLITRLLDTRLVHHNVTRWETFDVSPA VLRW--TREKQP NYGLAIEVTHL 241

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLIRDYG-----AQGDCDP 253  
 H G H + S+ P G G+ PL D R + P  
 Sbjct: 242 HQTRTHQGQHVRI--SRSLPQGSGDWAQLRPLLVTFGHDGRGHALTRHRRAKRSPKHHP 298

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQP 300  
 + + C R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 299 QRARKKNKNCRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344

tr Q9U5E8 Pf-BMP2/4 [Pf-bmp2/4] [Ptychoder a flava] 405 AA  
align

Score = 54.3 bits (129), Expect = 3e-06  
 Identities = 53/204 (25%), Positives = 86/204 (41%), Gaps = 14/204 (6%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAA--LHRHGRLSPRSAQARVTVEWLRVRDDGSNRTS-L 162  
 +P N + A LRL+ + + ++ + RS R+ V E L D+G L  
 Sbjct: 141 IPDNEVVTGAE RLRYCQGINI SS PMNT DDPSE YQFLHRINVHEILEPADEGGESIKRL 200

Query: 163 IDSRLVS VHE SGWKA FDVTEAVNFWXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRF 221  
 IDS++V + S W++FD+ AV W ++ VQ + P H +R  
 Sbjct: 201 IDSKVVDIRNSSWESFDIRPAVAKW KASQEE NHGVEVELTEV QNSQISPHKD--HVRLRR 258

Query: 222 ASQGAPAGLGE PQLELHTLDLIRDYGAQGDCDP EAPMTEGTR-----CCRQEMYIDLQGMK 276  
 +S A A + Q L D + +G R C R+ +Y+D +  
 Sbjct: 259 SSDLA-ASEWQRQRPLLITYTDDGKR PTRSKRN SERKKGGRK LKPNCRRSLYVDFSDVG 317

Query: 277 WAKNWVLEPPGFLAYECVGT CQQP 300  
 W +W++ PPG+ A+ C G C P  
 Sbjct: 318 W-NDWIVAPPGYNAFYCDGEC PFP 340

sp O46564 Bone morphogenetic protein 2 precursor (BMP-2) [BMP2] 395  
 BMP2\_RABBIT [Oryctolagus AA  
 cuniculus (Rabbit)] align

Score = 53.9 bits (128), Expect = 4e-06  
 Identities = 51/216 (23%), Positives = 85/216 (38%), Gaps = 44/216 (20%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAA-----LHRHGRLSPRSAQARVTVEWLRVRDDGS 157  
 +PP + A L++F+E + +A ++ + + P +A ++  
 Sbjct: 138 IPPEEFITS AELQV FREQM QEA LGDDSGFHH RINIYEIIKPATANSKFPA----- 187

Query: 158 NRTSLIDSRLVS VHE SGWKA FDVTEAVNFWXXXXXXXXXXXXVSVQREHLG-----PL 211  
 T L+D+RLV+ + S W++FDV T AV W V+ E G +  
 Sbjct: 188 --TRLLDTRLVNQNTSRWESFDVTPAVMRWTAQGHANHGFVVEVTHLEEKQGVSKRH VRI 245

Query: 212 ASGAHKLVRFASQGAPA-----GLGEPOLELHTLDLRDYGAQGDCDPEAPMTEGTRCC 264  
 + H SQ P G G P LH + R + + C  
 Sbjct: 246 SRSLHPDEHSWSQIRPLLVTFGHDGKGHP---LHRREKR----QAKHKQRKRLKSSCK 296

Query: 265 RQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTQQQP 300  
 R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 297 RHPLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 331

sp O19006 Bone morphogenetic protein 2 precursor (BMP-2) [BMP2] 396  
 BMP2\_DAMDA [Dama dama] AA  
 (Fallow deer) (Cervus dama) align

Score = 53.9 bits (128), Expect = 4e-06  
 Identities = 52/216 (24%), Positives = 87/216 (40%), Gaps = 44/216 (20%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHR---HGRLS-----PRSAQARVTVEWLVRDDGS 157  
 +P + A L++F + +P+A + H R++ P +A ++ V  
 Sbjct: 139 IPTEEFITSAELQVFGKHMPEALENNSSFHHRINIFEIIKPATANSKFPV----- 188

Query: 158 NRTSLIDSRLVS VHESGWKA F DVTEAVNFWXXXXXXXXXXXXVSVQREHLGP-----L 211  
 T L+D+RLV+ + S W++FDVT AV W V+ + G +  
 Sbjct: 189 --TRLLDTRLVTQN ASRWE SF DVT PAVMRWTAQGLTNHGFVVEAH PEDSYGASKRH VRI 246

Query: 212 ASGAHKLVRFASQGAPA-----GLGEPOLELHTLDLRDYGAQGDCDPEAPMTEGTRCC 264  
 + H+ SQ P G G P LH + R + + C  
 Sbjct: 247 SRSLHQDEHSWSQIRPLLVTFGHDGKGHP---LHRREKR----QAKHKQRKRLKSSCK 297

Query: 265 RQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTQQQP 300  
 R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 298 RHPLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 332

tr Q9PVK1 Anti-dorsalizing morphogenetic protein [ADM] [Gallus gallus] 364 AA  
 (Chicken) align

Score = 53.9 bits (128), Expect = 4e-06  
 Identities = 57/208 (27%), Positives = 82/208 (39%), Gaps = 41/208 (19%)

Query: 123 EPVPKAALHRHGR LSPRSAQARVTVEWL RV-----RDDGSNRTSLIDSRLVS VHES 173  
 E + A LH RL PR+A+ + +V D L+ +RL+S+ S  
 Sbjct: 102 EKILTAELHLF-RLWPRAAE GP RRHHFCQSVY QI LDESE PDSPEGQKL LATRLLS I QGS 160

Query: 174 GWKA F DVTEAVNFWXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAPAGLGE P 233  
 GW+ F +T+AV W V LG A A V+FAS G +P  
 Sbjct: 161 GWEVFAITQAVRDWTQDESSNRGLLTV----HGLGGSALEA-PAVQFASSGDHESKKP 215

Query: 234 QLELHTLDLRDYGAQGDCDPEAPM-----TEGTR-----CCRQEMYIDL 272  
 L L T D G +G P A + G R C R + +D  
 Sbjct: 216 MLVLFT----DDGRRGASLPMAGVPASQPRDFPAKLSGPRSARS LDR LQPCQRHPLSVDF 271

Query: 273 QGMKWAKNWVLEPPGFLAYECVGTQQQP 300  
 + + W+ W++ P G+ AY C G+C P

Sbjct: 272 EEIGWS-GWIISPRGYNAYHCRGSCPFP 298

sp P30884      **Bone morphogenetic protein 2-II precursor (BMP-2-II)**      398  
 BMPB\_XENLA [Xenopus  
 laevis (African clawed frog)]      AA  
align

Score = 53.1 bits (126), Expect = 8e-06  
 Identities = 55/211 (26%), Positives = 89/211 (42%), Gaps = 37/211 (17%)

Query: 109 PNSELV-QAVLRLFQE PVPK-----AALHR---HGRILSPRSAQARVTVEWLRVRDDGSN 158  
 P+ ELV + LR+F+E V + + LHR + + P+A+R V

Sbjct: 142 PDEELVTSSELRIFREQVQE PFKTDGSKLHRINIYDIVKPAAAASRGPV----- 190

Query: 159 RTSLIDSRLVSVHESGWKA F D VT E AVNFWXXXXXXXXXXXXVSVQREHLGPLASGAHKL 218  
 L+D+RL+ +ES W++FDVT A+ W V+ HL + +

Sbjct: 191 -VRLLDTRLIHHNESKWESFDVT PAITRWIAHKQPNHGFVVEVT---HLDNDTNVPKRH 245

Query: 219 VRFASQGAPAGLGE----PQLELHTLDLRDYGAQGD CDP EAPMTEGTR---CCRQEMY 269  
 VR S+ G P L + D + + +A + R C R +Y

Sbjct: 246 VRI-SRSLTLDKGHWPRIRPLLVTFSHDGKGHALHKRQKRQARHKQRKRLKSSCRRHPLY 304

Query: 270 IDLQGMKWAKNWVLEPPGFLAYECVGT CQQP 300  
 +D + W +W++ PPG+ A+ C G C P

Sbjct: 305 VDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 334

tr Q9VQG9      **CG16987-PA (Cg16987-pb) (GH14433p) [Alp23B]**      586 AA  
 [Drosophila  
 melanogaster (Fruit fly)]      align

Score = 53.1 bits (126), Expect = 8e-06  
 Identities = 33/109 (30%), Positives = 53/109 (48%), Gaps = 20/109 (18%)

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQ---QPPEALAFNPFL----- 311  
 T CCR+ +YI + + W+ NW+L+P G+ AY C G+C +A + + +

Sbjct: 481 TECCREHLYISFRDIGWS-NWILKPEGYNAYFCRGSCSSVASVTQAASHSSIMKILSTS 539

Query: 312 GPRQ-----CIASETASLPMIVSIKEGGRT RPQVVSLPNMRVQKCSC 353  
 G + C A + +SL ++V T V +LPNM V+ C C

Sbjct: 540 GANKSLELVPCCCTAKQYSSLQLVVMDSNTAT---VKTLPNMVVESCGC 585

sp O08717      **Inhibin beta E chain precursor (Activin beta-E chain)**      350  
 IHBE\_MOUSE [Inhbe] [Mus  
 musculus (Mouse)]      AA  
align

Score = 52.8 bits (125), Expect = 1e-05  
 Identities = 33/121 (27%), Positives = 54/121 (44%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQ-----QPPEALA 305  
 C+PE P+ CCR++ Y+D Q + W ++W+L+P G+ C G C P A +

Sbjct: 240 CEPEP TPL-----CCR RDHYVDFQELGW-RDWILQPEGYQLNYCSGQC PPHLAGSPGIAAS 293

Query: 306 FN-----WPFLGPRQCIASETASLPMIVSIKEGGRTGPQVVS LPNMRVQKCSC 353  
 F+ WP G C+ + L ++ G + V P+M V+ C C  
 Sbjct: 294 FHSAVFSLLKANNPWP-AGSSCCVPTARRPLSLLYLDHNGNVVKTDV---PDMVVEACGC 349

Query: 354 A 354  
 +  
 Sbjct: 350 S 350

sp P12643 Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A) 396  
 BMP2\_HUMAN [BMP2]  
 [Homo sapiens (Human)] align

Score = 52.8 bits (125), Expect = 1e-05  
 Identities = 53/216 (24%), Positives = 86/216 (39%), Gaps = 44/216 (20%)

Query: 107 LPPNSELVQAVRLRFQEPVPKAALHR---HGRLS-----PRSAQARVTVEWLRVRDDGS 157  
 +P + A L++F+E + A + H R++ P+A ++ V  
 Sbjct: 139 IPTEEFITSAELQVFREQMQLDALGNNSSFHHRINIYEIIKPATANSKFPV----- 188

Query: 158 NRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXVSVQREHLG-----PL 211  
 T L+D+RLV+ + S W++FDVT AV W V+ E G +  
 Sbjct: 189 --TRLLDTRLVNQNASRWESFDVTPAVMRWTAQGHANHGFVVEAHLEEKQGVSKRHVRI 246

Query: 212 ASGAHKLVRFASQGAPA-----GLGE PQLELHTLDLRDYGAQGDCDPEAPMTEGTRCC 264  
 + H+ SQ P G G P LH + R + + C  
 Sbjct: 247 SRSLHQDEHSWSQIRPLLVTFGHDGKGHP---LHKREKR-----QAKHKQRKRLKSSCK 297

Query: 265 RQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCAQQP 300  
 R +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 298 RHPLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 332

tr Q91XH3 Inhibin beta E [Inhbe] [Mus musculus (Mouse)] 350 AA align

Score = 52.8 bits (125), Expect = 1e-05  
 Identities = 33/121 (27%), Positives = 54/121 (44%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCAQPEAL 305  
 C+PE P+ CCR++ Y+D Q + W ++W+L+P G+ C G C P A +  
 Sbjct: 240 CEPETPL-----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 293

Query: 306 FN-----WPFLGPRQCIASETASLPMIVSIKEGGRTGPQVVS LPNMRVQKCSC 353  
 F+ WP G C+ + L ++ G + V P+M V+ C C  
 Sbjct: 294 FHSAVFSLLKANNPWP-AGSSCCVPTARRPLSLLYLDHNGNVVKTDV---PDMVVEACGC 349

Query: 354 A 354  
 +  
 Sbjct: 350 S 350

tr Q7Q3Q7 AgCP11289 (Fragment) [agCG50272] [Anopheles gambiae str. PEST] 459 AA

align

Score = 52.8 bits (125), Expect = 1e-05

Identities = 81/367 (22%), Positives = 137/367 (37%), Gaps = 63/367 (17%)

Query: 41 PVLDRADMEKLVIPAHVRAQYVVLLRRS-----HGDRSRGKRFQSFSREVAGRFLA 91

P + D K+VIP ++ Y ++ G +R +SF

Sbjct: 101 PNRPKIDRSKVVIPEAMKQLYAQIMGHDLVDSVSPKEGLNTRNANTVRSFTHEESHIDQ 160

Query: 92 SEASTHL--LVFGMEOQLPPNSELVQAVLRLFQEPPVKAALHRHGRLSRSAQARVTVEW 149  
H L+F + +P +L A L L +E + HR R R+ + +

Sbjct: 161 RFQHHHRFRLLFNVTS-IPRGEKLRAAEELTREGIA---HRSSRAQARTPVLYQVMVY 215

Query: 150 LRVRDDGSNRTS---LIDSRLVSVHESGWKAFCDVTEAVNFWXXXXXXXXXXXXXV---- 201  
VR + + L+D++ ++++ESG +FDV AV W V

Sbjct: 216 DIVRPGVKGKRAPTFLLVDTKTLAINESGTASFDVMPAVERWLRQPRKNHGLFVQVTGRG 275

Query: 202 -----SVQREHLGPLASGAHKLVRFASQGAPAGLG---EPQLELHTLD-----LRD 244  
S QR + P A H+ VR A +P L +T D +RD

Sbjct: 276 RGPPGHSRQRSSIVP-AVPVHEHVRLLRNAERHDHSVQKQPLLFTYTDDGRHKQRPIRD 334

Query: 245 YGAQGDCDPEAPMTEGTR----CCRQEMYIDLQGMKWAKNWLEPPGFLAYECVGTCAQ 299  
+ + A +R C R+ +Y+D + W +W++ PPG+ AY C G C+

Sbjct: 335 AISSANARRASAKRSSRRKNELCQRKPLYVDFSDVGW-NDWIVAPPGYEAYYCQGDCRF 393

Query: 300 P-----PEALAFNW-PFLGPRQCIASETASLPMIVSIKEGGTRPQVVSLPNM 346  
P + L ++ P L P+ C S ++ + E + + + + +M

Sbjct: 394 PIADHLNTTNHAIVQTLVNSYNPTLAPKACCVPTQLSSISMLYLNE--QNKVVLKNYQDM 451

Query: 347 RVQKCSC 353

V C C

Sbjct: 452 TVVGCSC 458

tr Q6PUC6 Decapentaplegic (Fragment) [Anopheles gambiae (African malaria mosquito)]

align

Score = 52.8 bits (125), Expect = 1e-05

Identities = 81/367 (22%), Positives = 137/367 (37%), Gaps = 63/367 (17%)

Query: 41 PVLDRADMEKLVIPAHVRAQYVVLLRRS-----HGDRSRGKRFQSFSREVAGRFLA 91

P + D K+VIP ++ Y ++ G +R +SF

Sbjct: 21 PNRPKIDRSKVVIPEAMKQLYAQIMGHDLVDSVSPKEGLNTRNANTVRSFTHEESHIDQ 80

Query: 92 SEASTHL--LVFGMEOQLPPNSELVQAVLRLFQEPPVKAALHRHGRLSRSAQARVTVEW 149  
H L+F + +P +L A L L +E + HR R R+ + +

Sbjct: 81 RFQHHHRFRLLFNVTS-IPRGEKLRAAEELTREGIA---HRSSRAQARTPVLYQVMVY 135

Query: 150 LRVRDDGSNRTS---LIDSRLVSVHESGWKAFCDVTEAVNFWXXXXXXXXXXXXXV---- 201  
VR + + L+D++ ++++ESG +FDV AV W V

Sbjct: 136 DIVRPGVKGKRAPTFLLVDTKTLAINESGTASFDVMPAVERWLRQPRKNHGLFVQVTGRG 195

Query: 202 -----SVQREHLGPLASGAHKLVRFASQGAPAGLG---EPQLELHTLD-----LRD 244  
S QR + P A H+ VR A +P L +T D +RD

Sbjct: 196 RGPPGHSRQRSSIVP-**AVPVHEHVRLLRNRNAAERHD**SWVQKQPLLFTYTDDGRHKQRPIRD 254  
 Query: 245 YGAQGDCDPEAPMTEGTR----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQ 299  
     + + A +R C R+ +Y+D + W +W++ PPG+ AY C G C+  
 Sbjct: 255 AISSANARRASAKRSSRRKNELCQRKPLYVDFSDVGW-NDWIVAPPGEAYYCQGDCRF 313  
 Query: 300 P-----PEALAFNW-PFLGPROCIASETASLPMIVSIKEGGRTTRPQVVSLPNM 346  
     P + L ++ P L P+ C S ++ + E + + + + +M  
 Sbjct: 314 PIADHLNTTNHAIVQTLVNSYNPTLAPKACCVPQLSSISMLYLNE--QNKVVLKNYQDM 371  
 Query: 347 RVQKCSC 353  
     V C C  
 Sbjct: 372 TVVGCSC 378

tr Q9W6T9 Activin beta B protein (Fragment) [inhbb] [Brachydanio rerio] 138 AA  
 (Zebrafish) (Danio rerio)

align

Score = 52.0 bits (123), Expect = 2e-05  
 Identities = 37/140 (26%), Positives = 62/140 (43%), Gaps = 25/140 (17%)

Query: 231 GEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLA 290  
     G QL+L L + G+ +CD G CCRQ+ YID + + W +W++ P G+  
 Sbjct: 1 GLEQLKLACLQVDSRGSGFECDGN---NGGLCCRQQFYIDFRLIGW-NDWIIAPAGYYG 55  
 Query: 291 YECVGTCAQQ----PPEALAFNWPFLGPRQ-----CIASETASLPMIVSIKEG 333  
     C G+C P A +F+ + + CI ++ +++ M+ E  
 Sbjct: 56 NYCEGSCPAYMAGVPGSASSFHTAVVNQYRMRGMSPGSVNCCIPTKLSTMSMLYFDDEY 115  
 Query: 334 GRTRPQVVSLPNMRVQKCSC 353  
     + V PNM V++C C  
 Sbjct: 116 NIVKRDV---PNMIVEECGC 132

tr Q9PWR8 Activin beta B subunit precursor [Carassius auratus] 392 AA  
 (Goldfish)

align

Score = 52.0 bits (123), Expect = 2e-05  
 Identities = 79/353 (22%), Positives = 131/353 (36%), Gaps = 66/353 (18%)

Query: 42 VLDRADMEKLVIPAHV--RAQYVVLRRSHGDRSR--GKRFQSFSREVAGRFLASEASTH 97  
     +L+R M + H +A V LR+ H + R G+ +F A E ++  
 Sbjct: 66 ILNRLQMRERPNIHPIPIPKAAMVTALRKIHAGKVREDGRVEIPNFDGHAAHNEVQEETSE 125  
 Query: 98 LLVFGMEQRLPPNSELVQAVLRLFQEP---VPKAALHRHGRSP---RSAQARVTVEWL 150  
     ++ F + P+ + ++ V +A L + +L P + + +VTV  
 Sbjct: 126 IISFAESDDVTPSKSSLYFLISNEGQNLYVLQANLWLYFKLLPGTQEKGRLRKVTVRVR 185

Query: 151 RVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFXXXXXXVSVQREHLGP 210  
     G N + + V + SGW F V+EAV RE L  
 Sbjct: 186 SYEPGGQNVHWPMMEKRVELKRSGWHTFPVSEAV-----REMLAK 225

Query: 211 LASGAHKLVRFASQGAPAG----LGEPQLELHTLDLRDYGAQGDCDP-----EAPMT 258

G + + +G A L +P H L Q D E T  
 Sbjct: 226 --GGRRQDLDIHCEGCEAANVLPILVDPSPSHRFLVVRAQQADSKHRIRKRGLECDGT 283

Query: 259 EGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQ----PPEALAFNWPFLGP 313  
 G CCRQ+ YID + + W +W++ P G+ C G+C P A +F+ +  
 Sbjct: 284 NGGLCCRCQQFYIDFRLIGW-NDWIIAPAGYYGNYCEGSCPAYMAGVPGSASSFHTAVVNQ 342

Query: 314 RQ-----CIASETASLPMIVSIKEGGRT RPQVVSLPNMRVQKCSCA 354  
 + CI ++ +++ M+ E + V PNM V++C CA  
 Sbjct: 343 YRMRGISPGSVNSCCIPTKLSTMSMLYFDDENIVKRDV---PNMIVEECGCA 392

tr Q869H8 GDF2 precursor [Crassostrea gigas (Pacific oyster)] 387 AA  
align

Score = 52.0 bits (123), Expect = 2e-05  
 Identities = 49/217 (22%), Positives = 85/217 (38%), Gaps = 31/217 (14%)

Query: 161 SLIDSRLVS VHESGWKA F D VT EA VN FW XXXXXXXXXX VS V Q RE HL GP LAS GA HK L VR 220  
 +L++SR + + GW+ FD+T+ V W + V G L + +  
 Sbjct: 179 TLVE SRT IDLS RDG WE IF DIT QDV QDW I EDPE LNNGIE--IF VD GLD AG QL VF PS LNITE 236

Query: 221 FASQ GAP AGL GE P Q L E L H T L D L R D Y G A -----QGD CDP-EAP MTEG-TRCC RQ E M Y I 270  
 S + P + L L+++ + Q D + + +G + R C C R I  
 Sbjct: 237 RMSSKS ST NTT I P N V I L P I L E M K T H E R S I L K R V K R Q N D I E R R D C V K G D G E S R C C R F T T I 296

Query: 271 DLQGMKWA KNW VLEPPGFLAYECVGT CQQPPEALAFNWPFLG-----PRQCI 317  
 + W +W+L PP + A+ C G+C P+ F G P+ C  
 Sbjct: 297 AFSDLGW-NDWILAPPDYEAHYCDGSC---PDRFKMANTFAGIQARLHALYPNKFPKPCC 352

Query: 318 ASETASLPMIVSIKEGGRT RPQVVSLPNMRVQKCSCA 354  
 S P+ + K+ + Q+ P+M V+ C CA  
 Sbjct: 353 VPSKLS-PLTILHKDSS-GKYQLTDYPDMIVEDCKCA 387

tr Q8MKC2 Bone morphogenetic protein 2 (Fragment) [Ovis aries (Sheep)] 223 AA  
align

Score = 51.6 bits (122), Expect = 2e-05  
 Identities = 41/154 (26%), Positives = 63/154 (40%), Gaps = 23/154 (14%)

Query: 160 TSLIDSRLVS VHESGWKA F D VT EA VN FW XXXXXXXXXX VS V Q RE HL GP-----LAS 213  
 T L+D+RLV+ + S W++FDVT AV W V+ + G ++  
 Sbjct: 42 TRLLDTRLVTQN ASRW ESFDVTPAVMRWT AQGLTNHGFVVAHPEDSHGASKRH VRIS R 101

Query: 214 GAHKLVRFA S Q G A P A -----GLGE P Q L E L H T L D L R D Y G A Q G D C D P E A P M T E G T R C C R Q 266  
 H+ SQ P G G P LH + R + + C R  
 Sbjct: 102 SLHQDEHSWSQIRPLLVTFGHDGKGHP---LHRREKR-----QAKHKQRKRLKSSCKRH 152

Query: 267 EMYIDLQGMKWA KNW VLEPPGFLAYECVGT CQQP 300  
 +Y+D + W +W++ PPG+ A+ C G C P  
 Sbjct: 153 PLYVDFSDVGW-NDWIVAPPGYHAFYCHGEC PFP 185

tr Q8IAE3 Sj-BMP2/4 [Sj-bmp2/4] [Stichopus japonicus (Sea cucumber)] 422 AA

align

Score = 51.2 bits (121), Expect = 3e-05

Identities = 62/250 (24%), Positives = 94/250 (36%), Gaps = 30/250 (12%)

Query: 80 QSFREVAGRFLASEA-STHLLVFGMEQRLLPPNSELVQAVLRLFQE PVP-----KAALHR 132  
+SF + F EA H LVF + + L A LRLF+ +P + AL+

Sbjct: 118 KSFHHIEEHFDIDEAIHRHRLVFNLS-IEENEELRLFRHAIPDHKIRKRHALNE 176

Query: 133 HGRLSPRSAQARVTVEWLRVRDDGSNRT---SLIDSRLVSVHESGWKA F DVTEAVNFWXX 189  
++ R+ + + ++ NR LIDS ++ V + W++ DV AV W

Sbjct: 177 SENITDGKVIQRINLYQI-LKPVARNRDVIKRLIDSI VIDVRNTTWE SLDVAPAVKSWTN 235

Query: 190 XXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAPAGLG-----EPQLELHT 239  
+ R P G L G A L P L +T

Sbjct: 236 DANSNYGVEIEIIDRRG--SPSRHGDDHLRTRRRIGDDASLEIHDEDQWFQQRPLLVTYT 293

Query: 240 LDLRDYGAQGD CDP EAPMTEGTR---CCRQEMYIDLQGMKWAKNWVLEPPGF LAYECVG 295  
D R + + R C + + Y+D + W +W+L P G+ AY C G

Sbjct: 294 DDGRTKRSKKRTKRQSKKKRRLKENCSKHS LYV DFAIVGW-DSWI LAPEGYQAYYCQG 352

Query: 296 TCQQP-PEAL 304

C P PE L

Sbjct: 353 ECPYPMPMPEHL 362

tr Q6XDQ0 Bone morphogenetic protein 2 [Gallus gallus (Chicken)] 392 AA

align

Score = 50.4 bits (119), Expect = 5e-05

Identities = 57/213 (26%), Positives = 86/213 (39%), Gaps = 41/213 (19%)

Query: 109 PNSELV-QAVLRLFQE PVPKAALHRHGR LSPRSAQARVTVEWLRVRDDGSNR---TSLID 164  
PN E V A L++F+E V +A S S R+ + + +++ T L+D

Sbjct: 136 PNEESVTS AELQI FREQVHEAFE-----SNSSYHHRINIYEIMKPATATSKDPVTRLLD 189

Query: 165 SRLVSVHESGWKA F DVTEAVNFWXXXXXXXVSVQREHLGPLASGAHKLVRF A-- 222  
+RLV + S W++FDVT AV W V+ HL S + + VR +

Sbjct: 190 TRLVHHNASKWESFDVTPAVLWIAHGQPNHGFV---VEVVHLDKENSASKRHVRISRS 245

Query: 223 -----SQGAPA-----GLGE P QLELHT L D L RDYGAQGD CDP EAPMTEGTRCCRQE 267  
SQ P G G P LH + R + C R

Sbjct: 246 LHQDEDSWSQLRPLLVTFGHDGKGHP---LHKREKRQ-----AKHKQRKRHKYSCKRHP 296

Query: 268 MYIDLQGMKWAKNWVLEPPGF LAYECVGTCQQP 300

+Y+D + W +W+ PPG+ A+ C G C P

Sbjct: 297 LYVDFNDVGW-NDWIVAPPGYSAFYCHGECPFP 328

sp P27093 Inhibin beta B chain precursor (Activin beta-B chain) 391  
IHBB\_CHICK [INHBB]  
[Gallus gallus (Chicken)] AA

align

Score = 50.1 bits (118), Expect = 6e-05

tr O13109 BMP2 [bmp2a] [Brachydanio rerio (Zebrafish) (Danio rerio)] 386 AA

align

Score = 50.1 bits (118), Expect = 6e-05

Identities = 68/252 (26%), Positives = 102/252 (39%), Gaps = 47/252 (18%)

Query: 65 LRRSHGDRSRGKRFQS FREVAGRFLASEASTHLLVFGMEQRLLPPNSELV-QAVLRLFQE 123  
 +R H D S S S R RFL + S P+ ELV A +R+F+E  
 Sbjct: 102 IRSFHHDESTEDPSSSSVRTTQ-RFLFNLT-----PDEELVTSADVRFRE 148

Query: 124 PVPKAALHRHGRLSPRSAQA-RVTVEWLRVRDDGSNR---TSLIDSRLVS VHESGWKAFD 179  
 + + L+ SA R+ V + +R GS + T L+D+RLV S W++FD  
 Sbjct: 149 QIVSS-----LNNASAGFHRINVHEI-IRPSGSLQEPITRLLDTRLVQHSLSKWEFD 200

Query: 180 VTEAVNFWXXXXXXXXXXXXXVSV---QREHLGPLASGAHKLVRFASQGAPA----- 228  
 VT AV W +S R+H+ ++ H SQ P  
 Sbjct: 201 VTPAVLKWT TDGHPNHGILVEISHPDQDSRKHVR-VSRSLHNNEDTWSQMRPLLVTYSHD 259

Query: 229 GLGE PQLELHTLDL RDYGAQGD CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGF 288  
 G G LH+ + R + + C R +Y+D + W +W++ PPG+  
 Sbjct: 260 GKGNV---LHSREKRQAR----NNKQRKKHKANCRRHSLYVDFSDVGW-NDWIVAPPY 310

Query: 289 LAYECVGT CQQP 300

A+ C G C P

Sbjct: 311 HAFYCQGECPFP 322

sp O88959 Inhibin beta E chain precursor (Activin beta-E chain) 350  
 IHBE\_RAT [Inhbe]  
 [Rattus norvegicus (Rat)]

AA

align

Score = 49.7 bits (117), Expect = 8e-05

Identities = 32/121 (26%), Positives = 53/121 (43%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPFLAYECVGT CQ----QPPEALA 305  
 C+ E P+ CCR++ Y+D Q + W ++W+L+P G+ C G C P A +  
 Sbjct: 240 CESETPL----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQC PPPHLAGSPGIAAS 293

Query: 306 FN-----WPFLGPRQCIASETASLPMIVSIKEGGTRPQVVSLPNMRVQKCSC 353  
 F+ WP G C+ + L ++ G + V P+M V+ C C  
 Sbjct: 294 FHSAVFSLLKANNPWP-AGSSCCVPTARRPLSLLYLDHNGNVVKTDV---PDMVVEACGC 349

Query: 354 A 354

+

Sbjct: 350 S 350

sp P17491 Inhibin beta B chain precursor (Activin beta-B chain) 411  
 IHBB\_RAT [Inhbb]  
 [Rattus norvegicus (Rat)]

AA

align

Score = 49.7 bits (117), Expect = 8e-05

Identities = 69/291 (23%), Positives = 117/291 (39%), Gaps = 45/291 (15%)

Query: 81 SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQE PVPKAALHRHGRLSPRS 140  
 SF E G LAS S L F + N +VQA L L+ + +P +  
 Sbjct: 149 SFAETDG--LAS--SRVRLYFFVSNEGQNLFVVQASLWLYLKLLPYVL-----EKG 196

Query: 141 AQARVTVEWLVRDDGSNRTSLIDSRLSVHESGWKAFDVTEAVNFWXXXXXXXXXXX 200  
 ++ +V V+ +R ++++ + V + SGW F +TEA+  
 Sbjct: 197 SRRKVRVKVYFQE QGHGDRWNVVEKK-VDLKRSGWHTFPITEAIQ---ALFERGERRLN 251

Query: 201 VSVQREHLGPLASGAHKLVRFASQGAPAGLGE PQLELHTLDLRDYGAQGDCDPEAPMTEG 260  
 + VQ + LA + P + + +L +R G + CD +  
 Sbjct: 252 LDVQCDSCQELAVVPVFVDPGEESH RPVVQARLGDSRHRIRKRGLE--CDGRTSL--- 306

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFAYECVGT CQQ----PPEALAFNWPFL---- 311  
 CCRQ+ +ID + + W +W++ P G+ C G+C P A +F+ +  
 Sbjct: 307 --CCRQQFFIDFRLIGW-NDWIIAPTGYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYR 363

Query: 312 -----GPRQ--CIASETASLPMIVSIKEGGTRPQVVSLPNMRVQKCSCA 354  
 GP CI ++ +S+ M+ E + V PNM V++C CA  
 Sbjct: 364 MRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDV--PNMIVEECGCA 411

sp Q04999 Inhibin beta B chain precursor (Activin beta-B chain) 367  
 IHBB\_MOUSE (Fragment) AA  
 [Inhbb] [Mus musculus (Mouse)] align

Score = 49.7 bits (117), Expect = 8e-05  
 Identities = 69/291 (23%), Positives = 117/291 (39%), Gaps = 45/291 (15%)

Query: 81 SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQE PVPKAALHRHGRLSPRS 140  
 SF E G LAS S L F + N +VQA L L+ + +P +  
 Sbjct: 105 SFAETDG--LAS--SRVRLYFFVSNEGQNLFVVQASLWLYLKLLPYVL-----EKG 152

Query: 141 AQARVTVEWLVRDDGSNRTSLIDSRLSVHESGWKAFDVTEAVNFWXXXXXXXXXXX 200  
 ++ +V V+ +R ++++ + V + SGW F +TEA+  
 Sbjct: 153 SRRKVRVKVYFQE QGHGDRWNVVEKK-VDLKRSGWHTFPITEAIQ---ALFERGERRLN 207

Query: 201 VSVQREHLGPLASGAHKLVRFASQGAPAGLGE PQLELHTLDLRDYGAQGDCDPEAPMTEG 260  
 + VQ + LA + P + + +L +R G + CD +  
 Sbjct: 208 LDVQCDSCQELAVVPVFVDPGEESH RPVVQARLGDSRHRIRKRGLE--CDGRTSL--- 262

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFAYECVGT CQQ----PPEALAFNWPFL---- 311  
 CCRQ+ +ID + + W +W++ P G+ C G+C P A +F+ +  
 Sbjct: 263 --CCRQQFFIDFRLIGW-NDWIIAPTGYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYR 319

Query: 312 -----GPRQ--CIASETASLPMIVSIKEGGTRPQVVSLPNMRVQKCSCA 354  
 GP CI ++ +S+ M+ E + V PNM V++C CA  
 Sbjct: 320 MRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDV--PNMIVEECGCA 367

sp O95393 Bone morphogenetic protein 10 precursor (BMP-10) [BMP10] 424  
 BM10\_HUMAN [Homo sapiens (Human)] AA align

Score = 49.7 bits (117), Expect = 8e-05  
 Identities = 50/235 (21%), Positives = 88/235 (37%), Gaps = 50/235 (21%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQARVT V-EWLRVRDDGS---NRTSL 162  
 +P + E++ A LRL+ L + R+ ++T+ E L + D N L

Sbjct: 134 IPHHEEVIMAE LRLY-----TLVQRDRMIYDG VDRKITIFEVLESKG DNEGERNMLVL 186

Query: 163 IDSRLV SVHESGW KAFDVTEAVNFW XXXXXXXXXX VSVQREHLGPLASGAHK---- 217  
 + + + S W+ FDVT+A+ W + + + +SG +

Sbjct: 187 VS GEIYGTN-SEWETFDVTDAIR RWQKS GSSTH QLEV HIESKHD EAEDASS GRLEID TSA 245

Query: 218 -----LVR FASQ GAPAGLGE PQL-----ELHTLDL RDYGAQGD CDP EAPM--- 257  
 L+ F+ + + +L EL L L + + + M

Sbjct: 246 QNKHNPL LIVFSDDQSSDKERKEELNEMISHEQLPE LDNLGLD SFSSGP GEEALLQMR SN 305

Query: 258 -----TEGTRCCRQEM YIDLQGMKWA KNWVLE PPGFLAYECVGTCQQP 300  
 +G C R +YID + + W +W++ PPG+ AYEC G C P

Sbjct: 306 IIYDSTARIRR NAKGN YCKRTPL YIDFKEIGW-DSWIIAPPGYEAYECRGVCNYP 359

sp P48969 DVR-1 protein homolog precursor [DVR1] [Strongylocentrotus 461 AA  
DVR1\_STRPU purpuratus (Purple sea urchin)]

align

Score = 49.3 bits (116), Expect = 1e-04  
 Identities = 50/226 (22%), Positives = 88/226 (38%), Gaps = 49/226 (21%)

Query: 106 RLPPNSELVQAVLRLFQE PVPKAALHRHGR LSPRSAQARVT VEWLRVR- DDGSNRTSLID 164  
 R+P + A LR+F++ R GR + R+ V LR R DGS +D

Sbjct: 189 RIPQGETV TS AELRV FRDA-----GRQGR-----SLYRIDVLLRERGSDGS RSPVYLD 237

Query: 165 SRLV SVHESGW KAFDVTEAVNFW XXXXXXXXXX V-SVQREHLGP----- 210  
 S +V + GW FD+T A + W V S+Q ++ P

Sbjct: 238 STIVGAGDH GWL VFDMTSATSTWRS YPGANV GLQLRVESLQGLN IDPTDAGVVGVGNNEG 297

Query: 211 -----LASGAH-KLVR FASQ GAPAGLGE PQL E LHTLDL RDYGAQGD CDP 254  
 +A+ +H+ R A+ G P+ D+ D

Sbjct: 298 REPFMVVF QRN EEVIA TN SHLRRN RRAATRQKKGGK PRKP DTDNDI-----ASRDSA 351

Query: 255 APMTEGTRCCRQEM YIDLQGMKWA KNWVLE PPGFLAYECVGTCQQP 300  
 + + +C R+ +++++ + + W + W++ P G++A+ C G C P

Sbjct: 352 SSLNSDWQCKRK NL FVN FEDLDW-QEWIIA PLGYV AFY C QGECAFP 396

tr Q90261 Activin beta B [inhbb] [Brachydanio rerio (Zebrafish) (Danio 393 AA  
 rerio)]

align

Score = 49.3 bits (116), Expect = 1e-04  
 Identities = 59/249 (23%), Positives = 94/249 (37%), Gaps = 63/249 (25%)

Query: 139 RSAQARVT VEWLR VRDDGS NRSLIDSRLV SVHESGW KAFDVTEAVNFW XXXXXXXXX 198  
 + +A+ VTV G N + + V + SGW F V+EA+

Sbjct: 175 KGLRAKVT VRVHS YEPGGQNVHWPMM EKRVELKRS GWHTFPVSEAI----- 220

Query: 199 XXVSVQREHLGPLASGAHKLVRFASQGAPAG----LGEPQLELHT--LDLRDYGAQG-- 249  
 RE L G + + +G A L +P H L +R A G  
 Sbjct: 221 -----REMLAK--GGRRQDLDIHCEGCEAANVLPILVDPSPSHRPFLVVRAQQADGKH 272

Query: 250 -----DCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTQ--- 299  
 +CD G CCRQ+ YID + + W +W++ P G+ C G+C  
 Sbjct: 273 RIRKRGLECDGN---NGGLCCRQQFYIDFRLIGW-NDWIIAPAGYYGNYCEGSCPAYMA 327

Query: 300 --PPEALAFNWPFLGPRQ-----CIASETASLPMIVSIKEGGRTQPQVSLPN 345  
 P A +F+ + + CI ++ +++ M+ E + V PN  
 Sbjct: 328 GVPGSASSFHTAVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDV---PN 384

Query: 346 MRVQKCSCA 354  
 M V++C CA  
 Sbjct: 385 MIVEECGCA 393

tr Q869H7 GDF3 precursor (Fragment) [Crassostrea gigas (Pacific oyster)] 251 AA

align

Score = 49.3 bits (116), Expect = 1e-04  
 Identities = 56/238 (23%), Positives = 95/238 (39%), Gaps = 57/238 (23%)

Query: 162 LIIDSRLVSVHESGWKA F DVTEAVNFXXXXXXV----SVQREHLGPLASGAH 216  
 +ID++ V +SGW+ FDVT AV W + SV L L H  
 Sbjct: 24 VIDTQHVVGRD S GWETFDV TS AV RRWVTKPSSSQILEIRIESVFHSVTDGDLDLTFEPQH 83

Query: 217 K----LVRFASQGAPAGLGE P QLELHTL DLRDYGAQGDC--DPEAPMT----- 258  
 K LV F++ + +L+LH + + + D D ++P++  
 Sbjct: 84 KNEPLL VVFSTD-----KQKLQLHKT ERHE LITRED SIYDIQSPLSGSKNSNNSLNET 136

Query: 259 -----EGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTQ--- 301  
 G C R+ M ++ ++W +W+L P + AYE CVG C P  
 Sbjct: 137 NTIGHKIHSRVKRRGRRSGGLCRRRPM TVNFADIQW-DSWI LAPSSYEAYE CVGKCHFPV 195

Query: 302 E---ALAFNWPFLGPRQ--CIASETASLPMIVSIKEGGRT-RPQVVS LPNMRVQKCSC 353  
 + + P PR+ C+ ++ S+ ++ + G T +P+ M V +C C  
 Sbjct: 196 NERLSPSL TMPKEYPRESCCVPTK LDSI S I LY DEYGV LTY KPK---YDGMVVTECGC 250

sp P09529 Inhibin beta B chain precursor (Activin beta-B chain) 407  
 IHBB\_HUMAN [INHBB] [Homo sapiens (Human)] AA  
align

Score = 48.5 bits (114), Expect = 2e-04  
 Identities = 67/291 (23%), Positives = 116/291 (39%), Gaps = 45/291 (15%)

Query: 81 SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQE P VP KA AL HR HG RLSPRS 140  
 SF E G LAS S L F + N + VQA L L + + P +  
 Sbjct: 145 SFAETDG--LAS--SRVRLYF FISNEGQNLFVVQASLWLYLKLPYVL-----EKG 192

Query: 141 AQARVTVEWL RVRDDGSNRTS LIDSRLVSVHESGWKA F DVTEAVNFXXXXXX 200  
 ++ +V V+ +R + + + R V + SGW F + TEA+  
 Sbjct: 193 SRRKVRVKVYFQE QGHGDRWNMVEKR-VDLKRSGWHTFPLTEAIQ---ALFERGERRLN 247

Query: 201 VSVQREHLGPLASGAHKLVRFASQGAPAGLGE P Q L E L H T L D L R D Y G A Q Q G D C D P E A P M T E G 260  
 + V Q + L A + P + + + L + R G + C D +  
 Sbjct: 248 LDVQCDSCQELAVVPVFVDPGEESHRFVVVQARLGDSRHRIRKRGLE--CDGRTNL--- 302

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQ----PPEALAFNWPFLGPRQ 315  
 CCRQ+ +ID + + W +W++ P G+ C G+C P A +F+ + +  
 Sbjct: 303 --CCRQQFFIDFRLIGW-NDWIIAPTGYGYCEGSCPAYLAGVPGSASSFHTAVVNQYR 359

Query: 316 -----CIASETASLPMIVSIKEGGGRTRPQVVS LPNMRVQKCSCA 354  
 CI ++ +++ M+ E + V PNM V++C CA  
 Sbjct: 360 MRGLNP GTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV---PNMIVEECGCA 407

tr Q9PTF9 Bone morphogenetic protein 7 [bmp7] [Brachydanio rerio] 432  
 (Zebrafish) AA  
 (Danio rerio)] align

Score = 48.5 bits (114), Expect = 2e-04  
 Identities = 46/173 (26%), Positives = 66/173 (37%), Gaps = 44/173 (25%)

Query: 162 LIDSRLVSVHESGWKA F D V T E A V N F W X X X X X X X X X V S V Q R ----- 205  
 L+DSR+V E GW FD+T N W V  
 Sbjct: 205 LLDSRVVWAEEGWL VFDLT VTSNH W V I N P G Q N L G Q L L V E T S H G A R M N P R R A G L V G S S G 264

Query: 206 -EHLGPL-----ASGAH-KLVRFASQG-----APAGLGE P Q L E L H T L D L R D Y G A 247  
 ++ P ASG H + VR AS G A G Q+ L T + + GA  
 Sbjct: 265 AQNKQPFMVAFLKASGIHLRSVR SASGGKQKGHHRTKNAKPGAAHSQVALKTAEATE-GA 323

Query: 248 QGD C D P E A P M T E G T R C C R Q E M Y I D L Q G M K W A K N W V L E P P G F L A Y E C V G T C Q Q P 300  
 DP+ C + E+Y+ + + W ++W++ P G+ AY C G C P  
 Sbjct: 324 S--IDPKQG-----CKKH ELYV SFRDLGW-QDWIIAPEGYAA YYCEGE CVFP 367

tr Q6EH35 Bone morphogenetic protein 2 (Fragment) [BMP-2] [Trachemys scripta] 285  
 (Red-eared slider turtle) (Pseudemys scripta)] AA  
 align

Score = 48.5 bits (114), Expect = 2e-04  
 Identities = 51/207 (24%), Positives = 83/207 (39%), Gaps = 29/207 (14%)

Query: 109 PNSE-LVQAVLRLFQE P VP KA AL HR HG RLSP RSAQ AR VT VE W L R V R D D G S N R T S L I D S R L 167  
 PN E L A L++F+E V + + + + + + + D + L+D+RL  
 Sbjct: 33 PNEEFLTSAELQIFREQVQETFENNSSYHHRINIYEIIIEAATATSKDPAAR---LLDTRL 89

Query: 168 VSVHESGWKA F D V T E A V N F W X X X X X X X V ----- SVQREHLGPLASGAHKLVR 220  
 V + S W++FDVT AV W V SV + H+ ++ H+  
 Sbjct: 90 VHQNASKWESFDVT PAVMRWIAHRQP NHGFIVEVVHLDNESSVSKRHVR-ISRSI HQDED 148

Query: 221 FASQGAPA-----GLGE P Q L E L H T L D L R D Y G A Q Q G D C D P E A P M T E G T R C C R Q E M Y I D L Q 273  
 SQ P G G H+L R+ + + + C R +Y+D  
 Sbjct: 149 SWSQLRPLLVTFGHDGKG-----HSLHKRE---KRQAKHKQRKRHKSSCKRHPLYVDFN 199

Query: 274 GMK WAKNWVLEPPGFLAYECVGT CQ Q P 300  
 + W +W++ PPG+ A+ C G C P

Sbjct: 200 DVGW-NDWIVAPPGYGAFYCHGECPFP 225

sp P58166 Inhibin beta E chain precursor (Activin beta-E chain) 350  
 IHBE\_HUMAN [INHBE] [Homo sapiens (Human)] AA align

Score = 48.1 bits (113), Expect = 2e-04  
 Identities = 31/121 (25%), Positives = 52/121 (42%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCA----QPPEALA 305  
 C+P P+ CCR++ Y+D Q + W ++W+L+P G+ C G C P A +  
 Sbjct: 240 CEPATPL----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 293

Query: 306 FN-----WPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353  
 F+ WP C+ + L++ G+ V P+M V+ C C  
 Sbjct: 294 FHSAVFSLLKANNPWP-ASTSCCVPTARRPLSLLYLDHNGNVVKTDV---PDMVVEACGC 349

Query: 354 A 354

+  
 Sbjct: 350 S 350

sp Q9R229 Bone morphogenetic protein 10 precursor (BMP-10) [Bmp10] 420  
 BM10\_MOUSE [Mus musculus (Mouse)] AA align

Score = 48.1 bits (113), Expect = 2e-04  
 Identities = 57/234 (24%), Positives = 89/234 (37%), Gaps = 51/234 (21%)

Query: 107 LPPNSELVQAVLRLFQEVPVKAALHRHGRLSRSAQARVTVEWLRVRDDGSN--RTSLID 164  
 +P + E+V A LRL+ L+ R+ ++T+ + DGS R+ L+  
 Sbjct: 133 IPHHEEVVMAELRLY-----TLVQRDRMMYDGVDRKITIFEVLESADGSEEERSMLV- 184

Query: 165 SRLVSVH---ESGWKAFDVTEAVNFWXxxxxxxxxxxVSQREHLGPLASGAHK--- 217  
 LVS S W+ FDVT+A W + ++ G +  
 Sbjct: 185 --LVSTEIYGTNSEWETFDVTATRRWQKSGPSTHQLEIHIESRQNQAEDTGRGQLEIDM 242

Query: 218 -----LVRFASQGAPAGLGEPQL-ELHT---LDLRDYGAQGDCDPEAPM----- 257  
 LV F+ + + +L EL T LDL D EA +  
 Sbjct: 243 SAQNKHDPPLLVSDDQSNDKEQKEELNELITHEQDLDLSDAFFSGPDEEALLQMRNSM 302

Query: 258 -----TEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCAQP 300  
 +G C + +YID + + W +W++ PPG+ AYEC G C P  
 Sbjct: 303 IDDSSTRIRRNAKGNYCKKTPLYIDFKEIGW-DSWIIAPPGYEAYECRGVCNYP 355

sp Q24735 60A protein precursor (Glass bottom boat protein) [gbb] 436  
 60A\_DROVI [Drosophila virilis (Fruit fly)] AA align

Score = 48.1 bits (113), Expect = 2e-04  
 Identities = 60/283 (21%), Positives = 103/283 (36%), Gaps = 47/283 (16%)

Query: 107 LPPNSELVQAVLRLFQE PVPKAALHRHGRILSPRSAQARVTVEWLRVRDDGSNRTSLIDSR 166  
 +P ++ L+ A LR++Q G+ + + Q VTV LR N + S  
 Sbjct: 164 IPTDNYLMMAELRIYQNS-----NEGKWTTNKQFTVTVYMLRSGGSAPNMLEPLSSV 216

Query: 167 LVSVHESGWKA FDVTEAVNFWXXXXXXXXXXXXXVSV---QREHLGPLASGAHKLVRFA 222  
 + GW +VTEA++ W +RE H+ +  
 Sbjct: 217 NTTG DYVGWLELNVTEALHDWRVNSNENHGIYIGAHALNKPEREIKLDDIGLIHRRTKVD 276

Query: 223 SQGAPAGLG-----EPQLELHTLDLRDYGAQGD CDP EAPMT-EGTRCCR 265  
 + P +G + + + TL R +P + E TR C+  
 Sbjct: 277 DENQP FMIGFFRGPELIKSTSGHSTQKRTKRSTLHQ RKKSKSEPVNPFIENS IENTRSCQ 336

Query: 266 -QEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQ PEA-----LAFNWPFL 311  
 Q +YID + + W +W++ P G+ A+ C G C P A + P  
 Sbjct: 337 MQTLYIDFKDLGW-HDWIIAPEGYGAFYCSGE CNFPLNAHMNATNHAIVQTLVHLLEPKR 395

Query: 312 GPRQCIA-SETASLP MIVSIKEGGTRPQVVSLPNMRVQKCSC 353  
 P+ C A + +LP++ + + + NM V+ C C  
 Sbjct: 396 VPKPCCAPTRL GALPVLYHLND---ENVNLKKYRN MIVKSCGC 435

tr Q9DG F1 Inhibin/activin (Fragment) [Cyprinus carpio (Common carp)] 115 AA

align

Score = 48.1 bits (113), Expect = 2e-04  
 Identities = 31/117 (26%), Positives = 52/117 (43%), Gaps = 21/117 (17%)

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGT CQQ-----PPEALAFNW 308  
 E T G CCRQ+ YID + + W +W++ P G+ C G+C P A +F+  
 Sbjct: 3 ECDGTNGGLCCRQFYIDFRLIGW-NDWIIAPEGYGYGNYCEGSCPAYMAGVPGSASSFHT 61

Query: 309 PFLGPRQ-----CIA SETASLP MIVSIKEGGTRPQVVSLPNMRVQKCSC 353  
 + + CI ++ +++ M+ E + V PNM V++C C  
 Sbjct: 62 AVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDV---PNMIVEECGC 115

Database: EXPASY/UniProt

Posted date: Nov 8, 2004 3:52 PM

Number of letters in database: 518,174,383

Number of sequences in database: 1,621,919

Lambda	K	H
0.322	0.136	0.436

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 366

length of database: 518,174,383

effective HSP length: 126

```
effective length of query: 240
effective length of database: 313,812,589
effective search space: 75315021360
effective search space used: 75315021360
T: 11
A: 40
X1: 16 ( 7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.9 bits)
S2: 74 (33.1 bits)
```



CLUSTAL W (1.74) multiple sequence alignment

## PileUp

MSF: 368 Type: P Check: 4364 ..

Name: sp|000292|TGF4\_HUMAN oo Len: 368 Check: 6379 Weight: 0.100  
 Name: sp|075610|LFTB\_HUMAN oo Len: 368 Check: 6179 Weight: 0.100  
 Name: tr|Q8BMF7 oo Len: 368 Check: 9710 Weight: 0.100  
 Name: sp|P57785|LFTB\_MOUSE oo Len: 368 Check: 9860 Weight: 0.100  
 Name: sp|Q64280|TGF4\_MOUSE oo Len: 368 Check: 2236 Weight: 0.100

//

sp|000292|TGF4\_HUMAN MWPLWLCWAL WVLPLAGPGA ALTEEQLLGS LLRQLQLSEV PVLDRADMEK  
 sp|075610|LFTB\_HUMAN MQPLWLCWAL WVLPLASPGA ALTGEQLLGS LLRQLQLKEV PTLDRADMEE  
 tr|Q8BMF7 MKSLWLWLCWAL WVLPLAGPGA AMTEEQVLSS LLQQLQLSQ A PTLDSADVEE  
 sp|P57785|LFTB\_MOUSE MKSLWLWLCWAL WVLPLAGPGA AMTEEQVLSS LLQQLQLSQ A PTLDSADVEE  
 sp|Q64280|TGF4\_MOUSE MPFLWLWLCWAL WALSLVSLRE ALTGEQILGS LLQQLQLDQP PVLDKADVEG

sp|000292|TGF4\_HUMAN LVI PAHVRAQ YV VLLRRSHG DR SRGKRFSQ SF REVAGRFL ASE ASTHLLV  
 sp|075610|LFTB\_HUMAN LVI PTHVRAQ YV ALLQRSHG DR SRGKRFSQ SF REVAGRFL ALE ASTHLLV  
 tr|Q8BMF7 MAI PTHVRSQ YV ALLQGSHA DR SRGKRFSQ NF REVAGRFL MSET STHLLV  
 sp|P57785|LFTB\_MOUSE MAI PTHVRSQ YV ALLQGSHA DR SRGKRFSQ NL REVAGRFL MSET STHLLV  
 sp|Q64280|TGF4\_MOUSE MVI PSHVRTQ YV ALLQHSHA SR SRGKRFSQ NL REVAGRFL VSET STHLLV

sp|000292|TGF4\_HUMAN FGME QRLPPN SELVQAVLRL FQE PVPKAAL HR HGR LSPRS AQ ARV TVEWL  
 sp|075610|LFTB\_HUMAN FGME QRLPPN SELVQAVI RL FQE PVPKAAL HR HGR LSPRS AR ARV TVEWL  
 tr|Q8BMF7 FGME QRLPPN SELVQAVLRL FQE PVPRTAL RR FER LSPHS AR ARV TIEWL  
 sp|P57785|LFTB\_MOUSE FGME QRLPPN SELVQAVLRL FQE PVPRTAL RR FER LSPHS AR ARV TIEWL  
 sp|Q64280|TGF4\_MOUSE FGME QRLPPN SELVQAVLRL FQE PVPRTAL RR QKR LSPHS AR ARV TIEWL

sp|000292|TGF4\_HUMAN RVRDDGSNRT SLIDSRLVSV HES GWKA FDV TE AVNF WQQL SR PRQ PLLLQ  
 sp|075610|LFTB\_HUMAN RVRDDGSNRT SLIDSRLVSV HES GWKA FDV TE AVNF WQQL SR PRQ PLLLQ  
 tr|Q8BMF7 RVREDGSNRT ALIDSRLVSI HES GWKA FDV TE AVNF WQQL SR PRQ PLLLQ  
 sp|P57785|LFTB\_MOUSE RVREDGSNRT ALIDSRLVSI HES GWKA FDV TE AVNF WQQL SR PRQ PLLLQ  
 sp|Q64280|TGF4\_MOUSE RFRDDGSNRT ALIDSRLVSI HES GWKA FDV TE AVNF WQQL SR PRQ PLLLQ

sp|000292|TGF4\_HUMAN VSVQREHLGP LASGAHKLVR FAS QGAP..A GLGE PQ LE LH TLD LR DY GAQ  
 sp|075610|LFTB\_HUMAN VSVQREHLGP LASGAHKLVR FAS QGAP..A GLGE PQ LE LH TLD LGD Y GAQ  
 tr|Q8BMF7 VSVQREHLGP GTWSAHKLVR FAA QGT PD GK GQ GE PQ LE LH TLD LKD Y GAQ  
 sp|P57785|LFTB\_MOUSE VSVQREHLGP GTWSAHKLVR FAA QGT PD GK GQ GE PQ LE LH TLD LKD Y GAQ  
 sp|Q64280|TGF4\_MOUSE VSVQREHLGP GTWSSHKLVR FAA QGT PD GK GQ GE PQ LE LH TLD LKD Y GAQ

sp|000292|TGF4\_HUMAN GD CDPEAPMT EGTRCCRQEM YIDLQGMKWA KNW VLE PPGF LAY ECV GTCQ  
 sp|075610|LFTB\_HUMAN GD CDPEAPMT EGTRCCRQEM YIDLQGMKWA ENW VLE PPGF LAY ECV GTCR  
 tr|Q8BMF7 GNCDPEPVPT EGTRCCRQEM YLDLQGMKWA ENW ILE PPGF LTY ECV GSCL  
 sp|P57785|LFTB\_MOUSE GNCDPEPVPT EGTRCCRQEM YLDLQGMKWA ENW ILE PPGF LTY ECV GSCL  
 sp|Q64280|TGF4\_MOUSE GNCDPEAPVT EGTRCCRQEM YLDLQGMKWA ENW ILE PPGF LTY ECV GSCL

sp|000292|TGF4\_HUMAN QPPEALAFNW PFLGPRQCIA SETASLPMIV SIKEGGTRP QVVSLPNMRV  
 sp|075610|LFTB\_HUMAN QPPEALAFKW PFLGPRQCIA SETDSLPMIV SIKEGGTRP QVVSLPNMRV

tr Q8BMF7	QLPESLTIGW PFLGPRQCVA SEMTSLPMIV SVKEGGRTGP QVVSLPNMRV
sp P57785 LFTB_MOUSE	QLPESLTIGW PFLGPRQCVA SEMTSLPMIV SVKEGGRTGP QVVSLPNMRV
sp Q64280 TGF4_MOUSE	QLPESLTSRW PFLGPRQCVA SEMTSLPMIV SVKEGGRTGP QVVSLPNMRV
sp O00292 TGF4_HUMAN	QKCSCASDGA LVPRRLQP
sp O75610 LFTB_HUMAN	QKCSCASDGA LVPRRLQP
tr Q8BMF7	QTCSCASDGA LIPRGIDL
sp P57785 LFTB_MOUSE	QTCSCASDGA LIPRGIDL
sp Q64280 TGF4_MOUSE	QTCSCASDGA LIPRRLQP